

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 10, 2005, 02:17:48 ; Search time 169 Seconds
(without alignments)
1741.566 Million cell updates/sec

Title: US-10-015-391A-277

Perfect score: 4031

Sequence: 1 MALPALGLDPWSLLGLFLFQ.....CRTSASDVDADNNCLGTEVA 761

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAY99418	standard;	protein;	761	AA.	
DE	Human PRO1317 (UNQ783) amino acid sequence SEQ ID NO:277.					
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH) GENENTECH INC.					
	Query Match	100.0%;	Score 4031;	DB 3;	Length 761;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 2						
ID	AAB24084	standard;	protein;	761	AA.	
DE	Human PRO1317 protein sequence SEQ ID NO:71.					
PN	WO200053755-A2.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
	Query Match	100.0%;	Score 4031;	DB 3;	Length 761;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 3						
ID	AAB66167	standard;	protein;	761	AA.	
DE	Protein of the invention #79.					
PN	WO200078961-A1.					
PD	28-DEC-2000.					
PA	(GETH) GENENTECH INC.					
	Query Match	100.0%;	Score 4031;	DB 4;	Length 761;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
RESULT 4						
ID	AAM80295	standard;	protein;	761	AA.	

DE Human protein SEQ ID NO 3947.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.

Query Match 100.0%; Score 4031; DB 4; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 5

ID AAB66043 standard; protein; 761 AA.
DE Human TANGO 265..
PN WO200077239-A2.
PD 21-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 100.0%; Score 4031; DB 4; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 6

ID ABG72615 standard; protein; 761 AA.
DE Human cytokine or cell proliferation/differentiation protein #5.
PN US2002137044-A1.
PD 26-SEP-2002.
PA (TANG/) TANG Y T.
PA (ZHOU/) ZHOU P.
PA (GOOD/) GOODRICH R.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (WEHR/) WEHRMAN T.
PA (YANG/) YANG Y.
PA (DRMA/) DRMANAC R T.

Query Match 100.0%; Score 4031; DB 6; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 7

ID ABU08366 standard; protein; 761 AA.
DE Amino acid sequence for human TANGO 265.
PN US2002182675-A1.
PD 05-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 100.0%; Score 4031; DB 6; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 8

ID ABO32703 standard; protein; 761 AA.
DE Secreted polypeptide-related protein #84.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.

Query Match 100.0%; Score 4031; DB 6; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 9

ID ABO33660 standard; protein; 761 AA.

DE Novel human secreted and transmembrane protein PRO1317.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 6; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 10
 ID ABO44513 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 11
 ID ABO33537 standard; protein; 761 AA.
 DE Novel human secreted and transmembrane protein PRO1317.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 12
 ID ADC18146 standard; protein; 761 AA.
 DE Human PRO polypeptide #79.
 PN US2003064925-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 13
 ID ADD70792 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003099625-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 14
 ID ADD39869 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003083462-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 15
 ID ADD70315 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003054406-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 16
 ID ADD38436 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.

PN US2003096955-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 17
 ID ADD39392 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003096954-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 18
 ID ADD38915 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003092061-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 19
 ID ADD40346 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003082627-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 20
 ID ADE50567 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003069179-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 21
 ID ADE20179 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003092883-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 22
 ID ADE50090 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003082626-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 23
 ID ADE21648 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003082628-A1.

PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 24
 ID ADF30073 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003204053-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 25
 ID ADF55966 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003204054-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 26
 ID ABU64394 standard; protein; 761 AA.
 DE Human Tango265 protein.
 PN WO2003080673-A1.
 PD 02-OCT-2003.
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 27
 ID ADH99470 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003065142-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 28
 ID ADE96650 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003195347-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 29
 ID ADF25961 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003199675-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 30
 ID ADF24860 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003198993-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 31
 ID ADF29596 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003203401-A1.
 PD 30-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 32
 ID ADE97127 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003195334-A1.
 PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 33
 ID ADH03165 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003216562-A1.
 PD 20-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 34
 ID ADH04119 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003220471-A1.
 PD 27-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 35
 ID ADH03642 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2003224478-A1.
 PD 04-DEC-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 36
 ID ADH04596 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2004005626-A1.
 PD 08-JAN-2004.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;

RESULT 37
 ID ADH61597 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2004014130-A1.
 PD 22-JAN-2004.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 38
 ID ADL94796 standard; protein; 761 AA.
 DE Human secreted/transmembrane protein PRO1317.
 PN US2004073015-A1.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 39
 ID ADQ10375 standard; protein; 761 AA.
 DE Human polypeptide #197.
 PN US2004121396-A1.
 PD 24-JUN-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 40
 ID ADQ98239 standard; protein; 761 AA.
 DE Human polypeptide #13.
 PN US6764677-B1.
 PD 20-JUL-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 41
 ID ADP25057 standard; protein; 761 AA.
 DE PRO polypeptide SEQ ID NO:2235.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 4031; DB 8; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 42
 ID AAE18211 standard; protein; 754 AA.
 DE Human MOL3b protein.
 PN WO200206339-A2.
 PD 24-JAN-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 99.2%; Score 3997; DB 5; Length 754;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 43
 ID ADD18200 standard; protein; 754 AA.
 DE Human molecule (MOL) protein MOL3b.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 99.2%; Score 3997; DB 7; Length 754;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 44
 ID AAB37984 standard; protein; 762 AA.
 DE Human secreted protein encoded by gene 1 clone HTDAA93.
 PN WO200055371-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 98.7%; Score 3980; DB 3; Length 762;

Best Local Similarity 98.9%; Pred. No. 0;

RESULT 45

ID AAE18210 standard; protein; 756 AA.

DE Human MOL3a protein.

PN WO200206339-A2.

PD 24-JAN-2002.

PA (CURA-) CURAGEN CORP.

Query Match 98.4%; Score 3966.5; DB 5; Length 756;

Best Local Similarity 98.7%; Pred. No. 0;

RESULT 46

ID ADD18198 standard; protein; 756 AA.

DE Human molecule (MOL) protein MOL3a.

PN WO2003003984-A2.

PD 16-JAN-2003.

PA (CURA-) CURAGEN CORP.

Query Match 98.4%; Score 3966.5; DB 7; Length 756;

Best Local Similarity 98.7%; Pred. No. 0;

RESULT 47

ID AAB66045 standard; protein; 730 AA.

DE Human TANGO 265 mature protein.

PN WO200077239-A2.

PD 21-DEC-2000.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 96.1%; Score 3875; DB 4; Length 730;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 48

ID ABO32705 standard; protein; 730 AA.

DE Secreted polypeptide-related protein #85.

PN US2003022279-A1.

PD 30-JAN-2003.

PA (FRAS/) FRASER C C.

PA (BARN/) BARNES T M.

PA (SHAR/) SHARP J D.

PA (KIRS/) KIRST S J.

PA (MYER/) MYERS P S.

PA (LEIB/) LEIBY K R.

PA (HOLT/) HOLTZMAN D A.

PA (MCCA/) MCCARTHY S A.

PA (WRIG/) WRIGHTON N.

PA (MACK/) MACKAY C R.

PA (GOOD/) GOODEARL A D J.

Query Match 96.1%; Score 3875; DB 6; Length 730;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 49

ID ADQ10377 standard; protein; 730 AA.

DE Human polypeptide #199.

PN US2004121396-A1.

PD 24-JUN-2004.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 96.1%; Score 3875; DB 8; Length 730;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 50

ID ADQ98241 standard; protein; 730 AA.

DE Human polypeptide #15.

PN US6764677-B1.

PD 20-JUL-2004.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 96.1%; Score 3875; DB 8; Length 730;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 51
 ID ABG79635 standard; protein; 730 AA.
 DE Human novel secreted protein SECP11, Incyte ID No. 7487507CD1.
 PN WO200262841-A2.
 PD 15-AUG-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 95.4%; Score 3847.5; DB 5; Length 730;
 Best Local Similarity 95.9%; Pred. No. 0;
 RESULT 52
 ID ABR43294 standard; protein; 728 AA.
 DE Human neurotransmission-associated protein NTRAN-24 SEQ ID NO:24.
 PN WO2003025129-A2.
 PD 27-MAR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 94.8%; Score 3821.5; DB 6; Length 728;
 Best Local Similarity 95.7%; Pred. No. 0;
 RESULT 53
 ID ADD67571 standard; protein; 762 AA.
 DE Human Ly667S protein SEQ ID NO:48.
 PN WO2003062401-A2.
 PD 31-JUL-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 94.5%; Score 3810.5; DB 7; Length 762;
 Best Local Similarity 94.0%; Pred. No. 0;
 RESULT 54
 ID ABU64393 standard; protein; 742 AA.
 DE Human Sema4A protein.
 PN WO2003080673-A1.
 PD 02-OCT-2003.
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 Query Match 93.3%; Score 3761.5; DB 7; Length 742;
 Best Local Similarity 94.1%; Pred. No. 0;
 RESULT 55
 ID ABM84900 standard; protein; 772 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5149.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 88.2%; Score 3555.5; DB 8; Length 772;
 Best Local Similarity 82.7%; Pred. No. 0;
 RESULT 56
 ID ABM84902 standard; protein; 772 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5151.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 88.2%; Score 3555.5; DB 8; Length 772;
 Best Local Similarity 82.7%; Pred. No. 0;
 RESULT 57
 ID ABM84903 standard; protein; 772 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5152.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 88.2%; Score 3555.5; DB 8; Length 772;

Best Local Similarity 82.7%; Pred. No. 0;
 RESULT 58
 ID ABM84899 standard; protein; 772 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5148.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 88.2%; Score 3555.5; DB 8; Length 772;
 Best Local Similarity 82.7%; Pred. No. 0;
 RESULT 59
 ID AAB66046 standard; protein; 652 AA.
 DE Human TANGO 265 extracellular domain.
 PN WO200077239-A2.
 PD 21-DEC-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 86.5%; Score 3486; DB 4; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 60
 ID ABO32706 standard; protein; 652 AA.
 DE Secreted polypeptide-related protein #86.
 PN US2003022279-A1.
 PD 30-JAN-2003.
 PA (FRAS/) FRASER C C.
 PA (BARN/) BARNES T M.
 PA (SHAR/) SHARP J D.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.
 PA (LEIB/) LEIBY K R.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (WRIG/) WRIGHTON N.
 PA (MACK/) MACKAY C R.
 PA (GOOD/) GOODEARL A D J.
 Query Match 86.5%; Score 3486; DB 6; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 61
 ID ADQ10378 standard; protein; 652 AA.
 DE Human polypeptide #200.
 PN US2004121396-A1.
 PD 24-JUN-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 86.5%; Score 3486; DB 8; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 62
 ID ADQ98242 standard; protein; 652 AA.
 DE Human polypeptide #16.
 PN US6764677-B1.
 PD 20-JUL-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 86.5%; Score 3486; DB 8; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0;
 RESULT 63
 ID ABM83444 standard; protein; 670 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3693.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.

Query Match 84.8%; Score 3418.5; DB 8; Length 670;
 Best Local Similarity 87.6%; Pred. No. 0;
 RESULT 64
 ID ABR43277 standard; protein; 631 AA.
 DE Human neurotransmission-associated protein NTRAN-7 SEQ ID NO:7.
 PN WO2003025129-A2.
 PD 27-MAR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 82.7%; Score 3333.5; DB 6; Length 631;
 Best Local Similarity 95.3%; Pred. No. 0;
 RESULT 65
 ID ADB64135 standard; protein; 629 AA.
 DE Human protein encoded by clone CTONG20017490.
 PN EP1308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 81.9%; Score 3300.5; DB 7; Length 629;
 Best Local Similarity 94.9%; Pred. No. 0;
 RESULT 66
 ID AAB66084 standard; protein; 760 AA.
 DE Murine semaphorin B protein.
 PN WO200077239-A2.
 PD 21-DEC-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 81.4%; Score 3280.5; DB 4; Length 760;
 Best Local Similarity 82.3%; Pred. No. 0;
 RESULT 67
 ID AAB66087 standard; protein; 760 AA.
 DE Murine protein: SEQ ID 76.
 PN WO200077239-A2.
 PD 21-DEC-2000.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 81.4%; Score 3280.5; DB 4; Length 760;
 Best Local Similarity 82.3%; Pred. No. 0;
 RESULT 68
 ID ABO32740 standard; protein; 760 AA.
 DE Secreted polypeptide-related protein #126.
 PN US2003022279-A1.
 PD 30-JAN-2003.
 PA (FRAS/) FRASER C C.
 PA (BARN/) BARNES T M.
 PA (SHAR/) SHARP J D.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.
 PA (LEIB/) LEIBY K R.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (WRIG/) WRIGHTON N.
 PA (MACK/) MACKAY C R.
 PA (GOOD/) GOODEARL A D J.
 Query Match 81.4%; Score 3280.5; DB 6; Length 760;
 Best Local Similarity 82.3%; Pred. No. 0;
 RESULT 69
 ID ABO32738 standard; protein; 760 AA.
 DE Secreted polypeptide-related protein #125.
 PN US2003022279-A1.

PD 30-JAN-2003.
 PA (FRAS/) FRASER C C.
 PA (BARN/) BARNES T M.
 PA (SHAR/) SHARP J D.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.
 PA (LEIB/) LEIBY K R.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (WRIG/) WRIGHTON N.
 PA (MACK/) MACKAY C R.
 PA (GOOD/) GOODEARL A D J.
 Query Match 81.4%; Score 3280.5; DB 6; Length 760;
 Best Local Similarity 82.3%; Pred. No. 0;
 RESULT 70
 ID ABU64396 standard; protein; 760 AA.
 DE Murine Sema4A protein.
 PN WO2003080673-A1.
 PD 02-OCT-2003.
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 Query Match 81.4%; Score 3280.5; DB 7; Length 760;
 Best Local Similarity 82.3%; Pred. No. 0;
 RESULT 71
 ID ADQ10421 standard; protein; 760 AA.
 DE Human polypeptide #235.
 PN US2004121396-A1.
 PD 24-JUN-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 81.4%; Score 3280.5; DB 8; Length 760;
 Best Local Similarity 82.3%; Pred. No. 0;
 RESULT 72
 ID ADQ10418 standard; protein; 760 AA.
 DE Human polypeptide #232.
 PN US2004121396-A1.
 PD 24-JUN-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 81.4%; Score 3280.5; DB 8; Length 760;
 Best Local Similarity 82.3%; Pred. No. 0;
 RESULT 73
 ID ADQ98290 standard; protein; 760 AA.
 DE Murine polypeptide #5.
 PN US6764677-B1.
 PD 20-JUL-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 81.4%; Score 3280.5; DB 8; Length 760;
 Best Local Similarity 82.3%; Pred. No. 0;
 RESULT 74
 ID ADQ98296 standard; protein; 760 AA.
 DE Murine polypeptide #7.
 PN US6764677-B1.
 PD 20-JUL-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 81.4%; Score 3280.5; DB 8; Length 760;
 Best Local Similarity 82.3%; Pred. No. 0;
 RESULT 75
 ID ABM84901 standard; protein; 764 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5150.

PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 80.2%; Score 3233.5; DB 8; Length 764;
 Best Local Similarity 77.2%; Pred. No. 0;
 RESULT 76
 ID ABM84895 standard; protein; 608 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5144.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 76.6%; Score 3088.5; DB 8; Length 608;
 Best Local Similarity 79.4%; Pred. No. 5.4e-306;
 RESULT 77
 ID ABM84898 standard; protein; 608 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5147.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 76.6%; Score 3088.5; DB 8; Length 608;
 Best Local Similarity 79.4%; Pred. No. 5.4e-306;
 RESULT 78
 ID ABM84896 standard; protein; 605 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5145.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 75.8%; Score 3056; DB 8; Length 605;
 Best Local Similarity 79.0%; Pred. No. 1.1e-302;
 RESULT 79
 ID ABU64395 standard; protein; 675 AA.
 DE Human Sema4A fusion protein.
 PN WO2003080673-A1.
 PD 02-OCT-2003.
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 Query Match 73.6%; Score 2968.5; DB 7; Length 675;
 Best Local Similarity 83.3%; Pred. No. 1.2e-293;
 RESULT 80
 ID ABM84897 standard; protein; 582 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5146.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 71.9%; Score 2896.5; DB 8; Length 582;
 Best Local Similarity 75.8%; Pred. No. 2.3e-286;
 RESULT 81
 ID AAM80301 standard; protein; 373 AA.
 DE Human protein SEQ ID NO 3959.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 43.6%; Score 1757.5; DB 4; Length 373;
 Best Local Similarity 92.1%; Pred. No. 3.9e-170;
 RESULT 82
 ID AAB93948 standard; protein; 328 AA.
 DE Human protein sequence SEQ ID NO:13974.
 PN EP1074617-A2.

PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 43.2%; Score 1743; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 9.5e-169;
RESULT 83
ID ABG66696 standard; protein; 328 AA.
DE Human novel polypeptide #31.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 43.1%; Score 1739; DB 5; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.4e-168;
RESULT 84
ID AAY99410 standard; protein; 837 AA.
DE Human PRO1480 (UNQ749) amino acid sequence SEQ ID NO:253.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 3; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 85
ID AAB66159 standard; protein; 837 AA.
DE Protein of the invention #71.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 4; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 86
ID AAU29250 standard; protein; 837 AA.
DE Human PRO polypeptide sequence #227.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 4; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 87
ID ABP65100 standard; protein; 837 AA.
DE Hypoxia-induced protein #26.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 31.6%; Score 1274; DB 5; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 88
ID ABU58626 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 89
ID ABU88174 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 90

ID ABU84489 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003032112-A1.

PD 13-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 91

ID ABR66363 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003027278-A1.

PD 06-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 92

ID ABR65753 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003036159-A1.

PD 20-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 93

ID ABU99693 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003040070-A1.

PD 27-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 94

ID ABU82932 standard; protein; 837 AA.

DE Human PRO polypeptide #227.

PN US2003032113-A1.

PD 13-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 95

ID ABU90053 standard; protein; 837 AA.

DE Novel human secreted and transmembrane protein PRO1480.

PN US2003036147-A1.

PD 20-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 96

ID ABR68302 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003027264-A1.

PD 06-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 97

ID ABU96355 standard; protein; 837 AA.

DE Novel human secreted and transmembrane protein PRO1480.

PN US2003036144-A1.

PD 20-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 98

ID ABU92786 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003036149-A1.
PD 20-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 99

ID ABO08863 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003044923-A1.
PD 06-MAR-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 100

ID ABO02915 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003040062-A1.
PD 27-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 101

ID ABR75069 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003040056-A1.
PD 27-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 102

ID ABR94831 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003044926-A1.
PD 06-MAR-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 103

ID ABU85804 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 104

ID ABU98964 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003013153-A1.
PD 16-JAN-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 105

ID ABU98179 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003017544-A1.
PD 23-JAN-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 106

ID ABU91885 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003027277-A1.
PD 06-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 107

ID ABR48242 standard; protein; 837 AA.
DE Human bladder cancer associated protein sequence SEQ ID NO:206.
PN WO2003003906-A2.
PD 16-JAN-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 108

ID ABU89578 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003036141-A1.
PD 20-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 109

ID ABU86419 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 110

ID ABU67632 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 111

ID ABU80660 standard; protein; 837 AA.
DE Human PRO protein #227.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 112

ID ABR99578 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003040063-A1.
PD 27-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 113

ID ABR98968 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003040064-A1.

PD 27-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 114

ID ABO16491 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003027267-A1.

PD 06-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 115

ID ABR92391 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003036160-A1.

PD 20-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 116

ID ABO19032 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003044925-A1.

PD 06-MAR-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 117

ID ABR78453 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003054474-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 118

ID ABU56640 standard; protein; 837 AA.

DE Lung cancer-associated polypeptide #233.

PN WO200286443-A2.

PD 31-OCT-2002.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 119

ID ABU85189 standard; protein; 837 AA.

DE Novel human secreted and transmembrane protein PRO1480.

PN US2003032114-A1.

PD 13-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 120

ID ABO00328 standard; protein; 837 AA.

DE Novel human secreted and transmembrane protein PRO1480.

PN US2003032101-A1.

PD 13-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 121

ID ABP97175 standard; protein; 837 AA.

DE Tumour-associated antigenic target protein TAT207 SEQ ID NO:57.

PN WO2003024392-A2.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 122
 ID ABO11660 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003036124-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 123
 ID ABO02305 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003040054-A1.
 PD 27-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 124
 ID ABU88879 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003036133-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 125
 ID ABU83574 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003036134-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 126
 ID ABO06375 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003022294-A1.
 PD 30-JAN-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 127
 ID ABR59411 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003027275-A1.
 PD 06-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 128
 ID ABO09473 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003027324-A1.
 PD 06-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 129
 ID ABO19337 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.

PN US2003036118-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 130
 ID ABO11355 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003036123-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 131
 ID ABR66973 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003036148-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 132
 ID ABO16186 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003040060-A1.
 PD 27-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 133
 ID ABO13892 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003044916-A1.
 PD 06-MAR-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 134
 ID ABU65795 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein, SEQ ID 454.
 PN US2003036156-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 135
 ID ABO07643 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003032117-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 136
 ID ABO03830 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003036128-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 137
 ID ABR67278 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003027266-A1.
 PD 06-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 138
 ID ABO15881 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003054483-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 139
 ID ABU56162 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein, PRO1480.
 PN US2003022298-A1.
 PD 30-JAN-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 140
 ID ABU65490 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003032102-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 141
 ID ABU95435 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003036117-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 142
 ID ABU71338 standard; protein; 837 AA.
 DE Human PRO1480 protein.
 PN US2003036143-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 143
 ID ABO07948 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003032130-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 144
 ID ABR70189 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003032138-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 145
 ID ABR69522 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 146
ID ABO01663 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 147
ID ABU81465 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 148
ID ABR60262 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 149
ID ABR67997 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 150
ID ABR65385 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 151
ID ABR68607 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 152
ID ABR72019 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 153

ID ABU85499 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003022295-A1.
 PD 30-JAN-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 154
 ID ABU89189 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003022297-A1.
 PD 30-JAN-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 155
 ID ABU83269 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003032105-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 156
 ID ABU95125 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003032123-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 157
 ID ABU90673 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003032108-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 158
 ID ABU84184 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003032111-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 159
 ID ABU93835 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003032119-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 160
 ID ABR65080 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003027263-A1.
 PD 06-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 161

ID ABR68912 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003027271-A1.
 PD 06-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 162
 ID ABO06728 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003036125-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 163
 ID ABR99273 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003040068-A1.
 PD 27-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 164
 ID ABU57157 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003027280-A1.
 PD 06-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 165
 ID ABU86109 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003022300-A1.
 PD 30-JAN-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 166
 ID ABU82396 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003036136-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 167
 ID ABU87407 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003036138-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 168
 ID ABU83879 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003032109-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 169
 ID ABO08253 standard; protein; 837 AA.

DE Human PRO polypeptide #227.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 170
ID ABU81964 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 171
ID ABU66128 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 172
ID ABR59957 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 173
ID ABU94145 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 174
ID ABO00018 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 175
ID ABR66668 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 176
ID ABR91086 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 177
ID ABU94513 standard; protein; 837 AA.

DE Human PRO polypeptide #227.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 178
ID ABU79395 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 179
ID ABU86724 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 180
ID ABU87029 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 181
ID ABU94818 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 182
ID ABO04745 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 183
ID ABR70494 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 184
ID ABU98659 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 185
ID ABR66058 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003036165-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 186
 ID ABR64775 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003027262-A1.
 PD 06-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 187
 ID ABU79700 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003032110-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 188
 ID ABU93091 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003036142-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 189
 ID ABU96050 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003036145-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 190
 ID ABU91270 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003036154-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 191
 ID ABU90363 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003036153-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 192
 ID ABO9778 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003044931-A1.
 PD 06-MAR-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 193
 ID ABO11050 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.

PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 194
ID ABR71104 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 195
ID ABU87712 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 196
ID ABU91580 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 197
ID ABU84794 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 198
ID ABR69884 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 199
ID ABU80261 standard; protein; 837 AA.
DE Human PRO protein #227.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 200
ID ABU93530 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 201
ID ABO10083 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003017543-A1.

PD 23-JAN-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 202
 ID ABO09168 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003036152-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 203
 ID ABU10736 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein #227.
 PN US2002127584-A1.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 204
 ID ABU95745 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003032115-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 205
 ID ABU96954 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003032140-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 206
 ID ABR70799 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003040076-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 207
 ID ABO05150 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003008352-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 208
 ID ABO08558 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003044922-A1.
 PD 06-MAR-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 209
 ID ABO05765 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 210
ID ABR74154 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 211
ID ABR95746 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 212
ID ABR81043 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 213
ID ABR81348 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 214
ID ABM01044 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 215
ID ABR88646 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 216
ID ABM77467 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003054479-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 217
 ID ABO28951 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068685-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 218
 ID ABO31696 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068725-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 219
 ID ABM08113 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068752-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 220
 ID ABO40593 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068682-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 221
 ID ABO36018 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003068701-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 222
 ID ABO44157 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003068755-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 223
 ID ADA78206 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003073180-A1.
 PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 224

ID ABM24952 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003104539-A1.
PD 05-JUN-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 225

ID ABO03220 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003036131-A1.
PD 20-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 226

ID ABR90476 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003040075-A1.
PD 27-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 227

ID ABM17390 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003054459-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 228

ID ABR95136 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003044930-A1.
PD 06-MAR-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 229

ID ABR95441 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003040071-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 230

ID ABO21679 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003054471-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 231

ID ABR97943 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003064452-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 232
 ID ABR87731 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068705-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 233
 ID ABM77772 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003054473-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 234
 ID ABM28002 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003064440-A1.
 PD 03-APR-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 235
 ID ABM06283 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068704-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 236
 ID ABM03789 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068722-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 237
 ID ABM35240 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003073183-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 238
 ID ABM26477 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104549-A1.
 PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 239

ID ABO48259 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003049749-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 240

ID ABR93001 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003064462-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 241

ID ABO24762 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003065159-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 242

ID ABM11773 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003064447-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 243

ID ABM02874 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003073184-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 244

ID ABM16170 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003064463-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 245

ID ABO27731 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003064451-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 246
 ID ABM29222 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068721-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 247
 ID ABM07198 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068699-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 248
 ID ABM21292 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068707-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 249
 ID ABM09638 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003073175-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 250
 ID ABO41508 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068695-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 251
 ID ABO36323 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003068703-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 252
 ID ABO43852 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003068732-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 253
 ID ABM76552 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003082717-A1.
 PD 01-MAY-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 254
 ID ABM76248 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104548-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 255
 ID ABM25867 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104542-A1.
 PD 05-JUN-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 256
 ID ABM26172 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104543-A1.
 PD 05-JUN-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 257
 ID ABO03525 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003036127-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 258
 ID ABO02610 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003040061-A1.
 PD 27-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 259
 ID ABR90781 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003036130-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 260
 ID ABR73849 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003054468-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 261

ID ABO17101 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 262

ID ABR94526 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003044917-A1.
PD 06-MAR-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 263

ID ABR76033 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003044929-A1.
PD 06-MAR-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 264

ID ABR71409 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 265

ID ABR93306 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 266

ID ABR93611 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 267

ID ABR88036 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 268

ID ABO33652 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 269
 ID ABO28036 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003064454-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 270
 ID ABO30171 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003064461-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 271
 ID ABO33380 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003068724-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 272
 ID ABM05068 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068727-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 273
 ID ABM09028 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068772-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 274
 ID ABO36628 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068714-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 275
 ID ABO35713 standard; protein; 837 AA.

DE Human PRO polypeptide #227.
 PN US2003068758-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 276
 ID ABO39678 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068776-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 277
 ID ABM10553 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003069407-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 278
 ID ABM12078 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104555-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 279
 ID ABO52224 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003049768-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 280
 ID ABO52529 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003049771-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 281
 ID ABO23847 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003032134-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 282
 ID ABR97333 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003054481-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 283
ID ABR87121 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 284
ID ABM11163 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 285
ID ABM28307 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 286
ID ABO32306 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 287
ID ABM15433 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 288
ID ABM06588 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 289
ID ABM04399 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068716-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 290
 ID ABM22512 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068740-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 291
 ID ABM07808 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068751-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 292
 ID ABO40898 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068684-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 293
 ID ABM35545 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003073179-A1.
 PD 17-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 294
 ID ABM33308 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003087374-A1.
 PD 08-MAY-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 295
 ID ABO52834 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003049773-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 296
 ID ABO50394 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049777-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 297
 ID ABU99388 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003040055-A1.
 PD 27-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 298
 ID ABO04440 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003036164-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 299
 ID ABO06070 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003040074-A1.
 PD 27-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 300
 ID ABM18610 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003054480-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 301
 ID ABR97638 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003059885-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 302
 ID ABR80738 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003049740-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 303
 ID ABM01349 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003049770-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 304
 ID ABR88951 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003073169-A1.
 PD 17-APR-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 305
 ID ABM13603 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003064457-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 306
 ID ABM20987 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068711-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 307
 ID ABO42118 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049745-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 308
 ID ABO42728 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049751-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 309
 ID ABM10248 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003067478-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 310
 ID ABO38763 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068773-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 311
 ID ABM33003 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003073185-A1.
 PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 312

ID ABM22817 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003087373-A1.

PD 08-MAY-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 313

ID ABM75028 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003096353-A1.

PD 22-MAY-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 314

ID ADA79998 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003073173-A1.

PD 17-APR-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 315

ID ABR96418 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003054458-A1.

PD 20-MAR-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 316

ID ABM02569 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003059886-A1.

PD 27-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 317

ID ABR86511 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003049758-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 318

ID ABR86816 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003049772-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 319

ID ABM16780 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 320
ID ABM29832 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 321
ID ABO29256 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 322
ID ABM24037 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 323
ID ABM23427 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 324
ID ABM22207 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 325
ID ABO37848 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 326
ID ABM28612 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 327
ID ABM28917 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 328
ID ABM66561 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 329
ID ABM75943 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 330
ID ABM34223 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 331
ID ABM34528 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 332
ID ABO20459 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 333
ID ABO21374 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 334

ID ABO22289 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 335

ID ABR96723 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 336

ID ABR85901 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 337

ID ABR99883 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 338

ID ABM00739 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 339

ID ABM00434 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 340

ID ABO29866 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 341

ID ABM23732 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003068736-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 342
 ID ABM29527 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068679-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 343
 ID ABO38458 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068767-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 344
 ID ABO45758 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003073182-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 345
 ID ABM20682 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104557-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 346
 ID ADA81725 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003092121-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 347
 ID ABO16796 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003027276-A1.
 PD 06-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 348
 ID ABO18422 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003044920-A1.
 PD 06-MAR-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 349

ID ABO22849 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003027265-A1.
PD 06-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 350

ID ABO23154 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 351

ID ABR92696 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 352

ID ABR81653 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 353

ID ABM78077 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 354

ID ABR89866 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003073171-A1.
PD 17-APR-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 355

ID ABM26782 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003032121-A1.
PD 13-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 356

ID ABM13908 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003064458-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 357
 ID ABO28646 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003064460-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 358
 ID ABO30476 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003064464-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 359
 ID ABM07503 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068702-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 360
 ID ABM04094 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068734-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 361
 ID ABO37238 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068719-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 362
 ID ABO41813 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068729-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 363
 ID ABO35408 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.

PN US2003068738-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 364
 ID ABM25257 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104540-A1.
 PD 05-JUN-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 365
 ID ABO47649 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049742-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 366
 ID ABO47954 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049747-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 367
 ID ABO48564 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049750-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 368
 ID ABO51614 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003049766-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 369
 ID ABO51919 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003049767-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 370
 ID ABO50699 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049779-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 371

ID ABR79823 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003040059-A1.

PD 27-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 372

ID ABM17085 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003040078-A1.

PD 27-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 373

ID ABO18117 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003044918-A1.

PD 06-MAR-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 374

ID ABO21069 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003032132-A1.

PD 13-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 375

ID ABR97028 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003054462-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 376

ID ABM12383 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003064445-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 377

ID ABM16475 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003064449-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 378

ID ABM24342 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003064441-A1.
 PD 03-APR-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 379
 ID ABM14823 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068696-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 380
 ID ABM04704 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068712-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 381
 ID ABM06893 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068730-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 382
 ID ABM09333 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003073174-A1.
 PD 17-APR-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 383
 ID ABO39373 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068775-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 384
 ID ABM75638 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104545-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 385
 ID ABM25562 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104541-A1.

PD 05-JUN-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 386

ID ABM20072 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003104554-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 387

ID ABO46978 standard; protein; 837 AA.

DE Human PRO polypeptide #227.

PN US2003049762-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 388

ID ABO47283 standard; protein; 837 AA.

DE Human PRO polypeptide #227.

PN US2003049765-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 389

ID ADA83523 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003049752-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 390

ID ABR71714 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003032133-A1.

PD 13-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 391

ID ABR72324 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003032136-A1.

PD 13-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 392

ID ABR98663 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003036129-A1.

PD 20-FEB-2003.

Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 393

ID ABO07033 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003040053-A1.
 PD 27-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 394
 ID ABR84986 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003040057-A1.
 PD 27-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 395
 ID ABR73544 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003054467-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 396
 ID ABR76638 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003044932-A1.
 PD 06-MAR-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 397
 ID ABR73239 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003027270-A1.
 PD 06-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 398
 ID ABM18305 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003054469-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 399
 ID ABO20764 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003032126-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 400
 ID ABO25507 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003054463-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 401
 ID ABO25812 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003054466-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 402
 ID ABR94221 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003059879-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 403
 ID ABR80128 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003049738-A1.
 PD 13-MAR-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 404
 ID ABM11468 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003064469-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 405
 ID ABO33075 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003064453-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 406
 ID ABO30781 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003064466-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 407
 ID ABO31086 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003064468-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 408

ID ABM27392 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068760-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 409
 ID ABM30137 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068769-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 410
 ID ABM05673 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003045700-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 411
 ID ABM15738 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068698-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 412
 ID ABM08723 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068759-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 413
 ID ABO42423 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049748-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 414
 ID ABO38153 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068765-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 415
 ID ABO46063 standard; protein; 837 AA.

DE Human PRO polypeptide #227.
 PN US2003049754-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 416
 ID ABM66866 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068688-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 417
 ID ADB20566 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003082767-A1.
 PD 01-MAY-2003.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 418
 ID ABM19767 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104552-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 419
 ID ABO49479 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049774-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 420
 ID ABO49784 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049775-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 421
 ID ADA78818 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003073181-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 6; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 422
 ID ABR88341 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068720-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 423
ID ABM27087 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 424
ID ABM03484 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 425
ID ABO39983 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 6; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 426
ID ABO50089 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 427
ID ABO51004 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 428
ID ABO05460 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 429
ID ABR74764 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 430
 ID ABO44505 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 431
 ID ABR77243 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003044927-A1.
 PD 06-MAR-2003.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 432
 ID ABM18000 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003040072-A1.
 PD 27-FEB-2003.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 433
 ID ABR96051 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003040073-A1.
 PD 27-FEB-2003.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 434
 ID ABO21984 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003054475-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 435
 ID ABO20154 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003032124-A1.
 PD 13-FEB-2003.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 436
 ID ABO24457 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003064467-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 437
 ID ABR86206 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003049759-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 438
ID ABM10858 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 439
ID ABM76857 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 440
ID ABR89561 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 441
ID ABM12688 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 442
ID ABM05978 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 443
ID ABO35103 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 444
ID ABM03179 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 445

ID ABM19157 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104550-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 446

ID ABM19462 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104551-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 447

ID ABO46673 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003049761-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 448

ID ABO49174 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049757-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 449

ID ABR69217 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003027273-A1.
 PD 06-FEB-2003.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 450

ID ABR89256 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003036119-A1.
 PD 20-FEB-2003.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 451

ID ABR72629 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003036120-A1.
 PD 20-FEB-2003.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 452

ID ABR74459 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003036161-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 453
 ID ABO18727 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003044921-A1.
 PD 06-MAR-2003.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 454
 ID ABR80433 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003049739-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 455
 ID ABM01654 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003059882-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 456
 ID ABM02264 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003059884-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 457
 ID ABR87426 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068687-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 458
 ID ABM12993 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003073186-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 459
 ID ABM30747 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003064443-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 460
ID ABM24647 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 461
ID ABO29561 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 462
ID ABO31391 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 463
ID ABM14518 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 464
ID ABM09943 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 465
ID ABO39068 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 466
ID ABM34833 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003104538-A1.
PD 05-JUN-2003.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 467
 ID ABO51309 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049781-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 468
 ID ABO04135 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003036158-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 469
 ID ABO10605 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003036151-A1.
 PD 20-FEB-2003.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 470
 ID ABR77848 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003040067-A1.
 PD 27-FEB-2003.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 471
 ID ABR79058 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003054456-A1.
 PD 20-MAR-2003.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 472
 ID ABO24152 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003054482-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 473
 ID ABR93916 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003054457-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 474
 ID ABM01959 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003059883-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 475
 ID ABM78382 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003049764-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 476
 ID ABO33529 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 477
 ID ABR90171 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003073177-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 478
 ID ABM27697 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003064442-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 479
 ID ABM13298 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003064450-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 480
 ID ABO32001 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068731-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 481
 ID ABM14213 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068683-A1.

PD 10-APR-2003.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 482

ID ABM08418 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003068754-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 483

ID ABO40288 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003068681-A1.

PD 10-APR-2003.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 484

ID ABM74723 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003096351-A1.

PD 22-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 485

ID ABM33918 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003096358-A1.

PD 22-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 486

ID ABM20377 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003104556-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 487

ID ABO48869 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003049756-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 488

ID ABR72934 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003036122-A1.

PD 20-FEB-2003.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 489

ID ABO15576 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 490

ID ABR85291 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 491

ID ABO15271 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 492

ID ABO17406 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 493

ID ABM17695 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 494

ID ABR85596 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 495

ID ABM77162 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 496

ID ABO28341 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003064459-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 497

ID ABM23122 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003068757-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 498

ID ABM30442 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003068723-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 499

ID ABM21902 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003068741-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 500

ID ABM21597 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003068744-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 501

ID ABM15128 standard; protein; 837 AA.

DE Human secreted polypeptide PRO1480, SEQ ID NO:454.

PN US2003068766-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 502

ID ABO41203 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003068694-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 503

ID ABO36933 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003068715-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 504

ID ABO37543 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003068726-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 505

ID ABM75333 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003104544-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 506

ID ABM33613 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003096357-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 507

ID ABO46368 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003049760-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 508

ID ADA82889 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein (PRO) #227.
 PN US2003049755-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 509

ID ABM31967 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068680-A1.
 PD 10-APR-2003.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 510

ID ABM31357 standard; protein; 837 AA.
 DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
 PN US2003068762-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 511

ID ADB86197 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 512

ID ABM32272 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 513

ID ABM32577 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 514

ID ABM31662 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 515

ID ABM31052 standard; protein; 837 AA.
DE Human secreted polypeptide PRO1480, SEQ ID NO:454.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 516

ID ADC18122 standard; protein; 837 AA.
DE Human PRO polypeptide #71.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 517

ID ADD05927 standard; protein; 837 AA.
DE Human secreted/transmembrane protein (PRO) #227.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 7; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 518

ID ADD70768 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003099625-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 519
 ID ADD39845 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003083462-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 520
 ID ADD70291 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003054406-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 521
 ID ADD38412 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003096955-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 522
 ID ADD39368 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003096954-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 523
 ID ADD38891 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003092061-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 524
 ID ADD40322 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003082627-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 525
 ID ADE50543 standard; protein; 837 AA.

DE Human secreted/transmembrane protein PRO1480.
 PN US2003069179-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 526
 ID ADE20155 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003092883-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 527
 ID ADE50066 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003082626-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 528
 ID ADE21624 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003082628-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 529
 ID ADF30049 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003204053-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 530
 ID ADF55942 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003204054-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 531
 ID ADG02922 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003207397-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 532
 ID ADG01629 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.

PN US2003207399-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 533
 ID ADF95804 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003207398-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 534
 ID ADG12619 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003207392-A1.
 PD 06-NOV-2003.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 535
 ID ADH09279 standard; protein; 837 AA.
 DE Human PRO polypeptide #227.
 PN US2003207395-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 536
 ID ADH99446 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2003065142-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 537
 ID ADL33058 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003207396-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 538
 ID ADM30594 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2003073813-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 7; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 539
 ID ADN38875 standard; protein; 837 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:193.
 PN WO2003042661-A2.
 PD 22-MAY-2003.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 540

ID ADN39893 standard; protein; 837 AA.

DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C263.

PN WO2003042661-A2.

PD 22-MAY-2003.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 31.6%; Score 1274; DB 7; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 541

ID ADE74591 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003211572-A1.

PD 13-NOV-2003.

Query Match 31.6%; Score 1274; DB 8; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 542

ID ADE75203 standard; protein; 837 AA.

DE Human secreted/transmembrane protein (PRO) #227.

PN US2003211574-A1.

PD 13-NOV-2003.

Query Match 31.6%; Score 1274; DB 8; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 543

ID ADE96626 standard; protein; 837 AA.

DE Human secreted/transmembrane protein PRO1480.

PN US2003195347-A1.

PD 16-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 8; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 544

ID ADF25937 standard; protein; 837 AA.

DE Human secreted/transmembrane protein PRO1480.

PN US2003199675-A1.

PD 23-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 8; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 545

ID ADF24836 standard; protein; 837 AA.

DE Human secreted/transmembrane protein PRO1480.

PN US2003198993-A1.

PD 23-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 8; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 546

ID ADF29572 standard; protein; 837 AA.

DE Human secreted/transmembrane protein PRO1480.

PN US2003203401-A1.

PD 30-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 31.6%; Score 1274; DB 8; Length 837;

Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 547

ID ADE97103 standard; protein; 837 AA.
DE Human secreted/transmembrane protein PRO1480.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 548

ID ADF96416 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 549

ID ADG04687 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 550

ID ADG00847 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 551

ID ADG83103 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 552

ID ADH03141 standard; protein; 837 AA.
DE Human secreted/transmembrane protein PRO1480.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 553

ID ADH04095 standard; protein; 837 AA.
DE Human secreted/transmembrane protein PRO1480.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;

RESULT 554

ID ADH03618 standard; protein; 837 AA.

DE Human secreted/transmembrane protein PRO1480.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 555
ID ADH26384 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 556
ID ADH33353 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 557
ID ADH04572 standard; protein; 837 AA.
DE Human secreted/transmembrane protein PRO1480.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 558
ID ADH61573 standard; protein; 837 AA.
DE Human secreted/transmembrane protein PRO1480.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 559
ID ADJ55092 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 560
ID ADJ64863 standard; protein; 837 AA.
DE Human PRO polypeptide #227.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 31.6%; Score 1274; DB 8; Length 837;
Best Local Similarity 38.9%; Pred. No. 4.6e-120;
RESULT 561
ID ADM31759 standard; protein; 837 AA.
DE Novel human secreted and transmembrane protein PRO1480.

PN US2004048334-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 8; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 562
 ID ADM36806 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2004053358-A1.
 PD 18-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 8; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 563
 ID ADM40611 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2004048335-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 8; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 564
 ID ADL94772 standard; protein; 837 AA.
 DE Human secreted/transmembrane protein PRO1480.
 PN US2004073015-A1.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 8; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 565
 ID ADN38219 standard; protein; 837 AA.
 DE Novel human secreted and transmembrane protein PRO1480.
 PN US2004091959-A1.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 8; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 566
 ID ABM81667 standard; protein; 837 AA.
 DE Tumour-associated antigenic target (TAT) polypeptide PRO82495, SEQ:4308.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 31.6%; Score 1274; DB 8; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.6e-120;
 RESULT 567
 ID ABB97964 standard; protein; 893 AA.
 DE Human protein sequence #31.
 PN WO200252005-A1.
 PD 04-JUL-2002.
 PA (KAZU-) KAZUSA DNA RES INST FOUND.
 PA (CELE-) CELESTAR LEXICO-SCI LTD.
 Query Match 31.6%; Score 1274; DB 5; Length 893;
 Best Local Similarity 38.9%; Pred. No. 5.1e-120;
 RESULT 568
 ID AAE03818 standard; protein; 832 AA.
 DE Human gene 1 encoded secreted protein HKAHL26, SEQ ID NO: 64.

PN WO200136440-A1.
 PD 25-MAY-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 31.5%; Score 1271.5; DB 4; Length 832;
 Best Local Similarity 39.1%; Pred. No. 8.1e-120;
 RESULT 569
 ID ABG64522 standard; protein; 832 AA.
 DE Human albumin fusion protein #1197.
 PN WO200177137-A1.
 PD 18-OCT-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 31.5%; Score 1271.5; DB 5; Length 832;
 Best Local Similarity 39.1%; Pred. No. 8.1e-120;
 RESULT 570
 ID ADL77789 standard; protein; 832 AA.
 DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1271.
 PN US2004010134-A1.
 PD 15-JAN-2004.
 PA (ROSE/) ROSEN C A.
 PA (HASE/) HASELTINE W A.
 Query Match 31.5%; Score 1271.5; DB 8; Length 832;
 Best Local Similarity 39.1%; Pred. No. 8.1e-120;
 RESULT 571
 ID ADQ37648 standard; protein; 837 AA.
 DE Human SEMA4B protein SEQ ID NO:1.
 PN WO2004058817-A1.
 PD 15-JUL-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 31.1%; Score 1255; DB 8; Length 837;
 Best Local Similarity 38.6%; Pred. No. 4e-118;
 RESULT 572
 ID ADQ37654 standard; protein; 837 AA.
 DE Human SEMA4B-M2 protein SEQ ID NO:7.
 PN WO2004058817-A1.
 PD 15-JUL-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 31.1%; Score 1255; DB 8; Length 837;
 Best Local Similarity 38.6%; Pred. No. 4e-118;
 RESULT 573
 ID ADQ37657 standard; protein; 837 AA.
 DE Human SEMA4B-M3 protein SEQ ID NO:10.
 PN WO2004058817-A1.
 PD 15-JUL-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 31.1%; Score 1254; DB 8; Length 837;
 Best Local Similarity 38.6%; Pred. No. 5.1e-118;
 RESULT 574
 ID ADQ37651 standard; protein; 837 AA.
 DE Human SEMA4B-M1 protein SEQ ID NO:4.
 PN WO2004058817-A1.
 PD 15-JUL-2004.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 31.0%; Score 1251; DB 8; Length 837;
 Best Local Similarity 38.6%; Pred. No. 1e-117;
 RESULT 575
 ID AAU77413 standard; protein; 791 AA.
 DE Human NOV7 protein, homologue of semaphorin proteins.

PN WO200206329-A2.
 PD 24-JAN-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 30.7%; Score 1239; DB 5; Length 791;
 Best Local Similarity 39.1%; Pred. No. 1.6e-116;
 RESULT 576
 ID ADJ76370 standard; protein; 782 AA.
 DE Marker gene related amino acid sequence SEQ ID NO:1622.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Query Match 29.7%; Score 1198.5; DB 8; Length 782;
 Best Local Similarity 39.9%; Pred. No. 2.2e-112;
 RESULT 577
 ID ABG33005 standard; protein; 261 AA.
 DE Semaphorin protein B28.71.
 PN CN1342663-A.
 PD 03-APR-2002.
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 Query Match 29.0%; Score 1168.5; DB 5; Length 261;
 Best Local Similarity 39.1%; Pred. No. 4e-110;
 RESULT 578
 ID ABB97963 standard; protein; 886 AA.
 DE Human protein sequence #30.
 PN WO200252005-A1.
 PD 04-JUL-2002.
 PA (KAZU-) KAZUSA DNA RES INST FOUND.
 PA (CELE-) CELESTAR LEXICO-SCI LTD.
 Query Match 27.2%; Score 1097; DB 5; Length 886;
 Best Local Similarity 36.6%; Pred. No. 6.5e-102;
 RESULT 579
 ID ADR67094 standard; protein; 886 AA.
 DE Human cancer associated protein sequence SEQ ID NO:140.
 PN WO2004074321-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 27.2%; Score 1097; DB 8; Length 886;
 Best Local Similarity 36.6%; Pred. No. 6.5e-102;
 RESULT 580
 ID AAE03640 standard; protein; 833 AA.
 DE Human extracellular matrix and cell adhesion molecule-4 (XMAD-4).
 PN WO200142285-A2.
 PD 14-JUN-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 27.1%; Score 1094; DB 4; Length 833;
 Best Local Similarity 37.2%; Pred. No. 1.2e-101;
 RESULT 581
 ID ADI28039 standard; protein; 833 AA.
 DE ECMCAD protein 7950094CD1.
 PN WO200202634-A2.
 PD 10-JAN-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 27.0%; Score 1090; DB 5; Length 833;
 Best Local Similarity 37.1%; Pred. No. 3.1e-101;
 RESULT 582
 ID ADR67100 standard; protein; 833 AA.
 DE Human cancer associated protein sequence SEQ ID NO:146.

PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 27.0%; Score 1090; DB 8; Length 833;
Best Local Similarity 37.1%; Pred. No. 3.1e-101;
RESULT 583
ID AAE18213 standard; protein; 833 AA.
DE Human MOL5a protein..
PN WO200206339-A2.
PD 24-JAN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 26.9%; Score 1084; DB 5; Length 833;
Best Local Similarity 37.0%; Pred. No. 1.3e-100;
RESULT 584
ID ADD18204 standard; protein; 833 AA.
DE Human molecule (MOL) protein MOL5a.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 26.9%; Score 1084; DB 7; Length 833;
Best Local Similarity 37.0%; Pred. No. 1.3e-100;
RESULT 585
ID AAE18214 standard; protein; 833 AA.
DE Human MOL5b protein.
PN WO200206339-A2.
PD 24-JAN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 26.9%; Score 1083; DB 5; Length 833;
Best Local Similarity 37.3%; Pred. No. 1.6e-100;
RESULT 586
ID AAE18215 standard; protein; 833 AA.
DE Human MOL5c protein.
PN WO200206339-A2.
PD 24-JAN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 26.9%; Score 1083; DB 5; Length 833;
Best Local Similarity 37.3%; Pred. No. 1.6e-100;
RESULT 587
ID ADD18208 standard; protein; 833 AA.
DE Human molecule (MOL) protein MOL5c.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 26.9%; Score 1083; DB 7; Length 833;
Best Local Similarity 37.3%; Pred. No. 1.6e-100;
RESULT 588
ID ADD18206 standard; protein; 833 AA.
DE Human molecule (MOL) protein MOL5b.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 26.9%; Score 1083; DB 7; Length 833;
Best Local Similarity 37.3%; Pred. No. 1.6e-100;
RESULT 589
ID ADG76093 standard; protein; 833 AA.
DE Human NOVX protein to treat human pathological conditions (SeqID 6).
PN WO2003085096-A2.

PD 16-OCT-2003.

PA (CURA-) CURAGEN CORP.

Query Match 26.9%; Score 1083; DB 7; Length 833;

Best Local Similarity 37.3%; Pred. No. 1.6e-100;

RESULT 590

ID AAB61238 standard; protein; 834 AA.

DE Murine M-Sema-F protein.

PN WO200100638-A2.

PD 04-JAN-2001.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 26.8%; Score 1079.5; DB 4; Length 834;

Best Local Similarity 35.4%; Pred. No. 3.6e-100;

RESULT 591

ID ABO32675 standard; protein; 834 AA.

DE Secreted polypeptide-related protein #118.

PN US2003022279-A1.

PD 30-JAN-2003.

PA (FRAS/) FRASER C C.

PA (BARN/) BARNES T M.

PA (SHAR/) SHARP J D.

PA (KIRS/) KIRST S J.

PA (MYER/) MYERS P S.

PA (LEIB/) LEIBY K R.

PA (HOLT/) HOLTZMAN D A.

PA (MCCA/) MCCARTHY S A.

PA (WRIG/) WRIGHTON N.

PA (MACK/) MACKAY C R.

PA (GOOD/) GOODEARL A D J.

Query Match 26.8%; Score 1079.5; DB 6; Length 834;

Best Local Similarity 35.4%; Pred. No. 3.6e-100;

RESULT 592

ID ADB90780 standard; protein; 834 AA.

DE Mouse M-Sema-F protein.

PN US2003082586-A1.

PD 01-MAY-2003.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 26.8%; Score 1079.5; DB 7; Length 834;

Best Local Similarity 35.4%; Pred. No. 3.6e-100;

RESULT 593

ID ADF71515 standard; protein; 834 AA.

DE Murine M-Sema-F.

PN US2003175733-A1.

PD 18-SEP-2003.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 26.8%; Score 1079.5; DB 7; Length 834;

Best Local Similarity 35.4%; Pred. No. 3.6e-100;

RESULT 594

ID ADQ10333 standard; protein; 834 AA.

DE Human polypeptide #169.

PN US2004121396-A1.

PD 24-JUN-2004.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 26.8%; Score 1079.5; DB 8; Length 834;

Best Local Similarity 35.4%; Pred. No. 3.6e-100;

RESULT 595

ID ADR67091 standard; protein; 834 AA.

DE Mouse cancer associated protein sequence SEQ ID NO:137.

PN WO2004074321-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 26.8%; Score 1079.5; DB 8; Length 834;
 Best Local Similarity 35.4%; Pred. No. 3.6e-100;
 RESULT 596
 ID ADG76099 standard; protein; 833 AA.
 DE Human NOVX protein to treat human pathological conditions (SeqID 12).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 26.7%; Score 1076; DB 7; Length 833;
 Best Local Similarity 36.8%; Pred. No. 8.3e-100;
 RESULT 597
 ID ADG76089 standard; protein; 634 AA.
 DE Human NOVX protein to treat human pathological conditions (SeqID 2).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 26.6%; Score 1071; DB 7; Length 634;
 Best Local Similarity 39.1%; Pred. No. 1.7e-99;
 RESULT 598
 ID ADD18234 standard; protein; 634 AA.
 DE Human molecule (MOL) protein MOL5d.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 26.5%; Score 1067; DB 7; Length 634;
 Best Local Similarity 39.1%; Pred. No. 4.4e-99;
 RESULT 599
 ID ADD18237 standard; protein; 638 AA.
 DE Human molecule (MOL) protein MOL5e.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 26.5%; Score 1067; DB 7; Length 638;
 Best Local Similarity 39.1%; Pred. No. 4.4e-99;
 RESULT 600
 ID ADG76095 standard; protein; 638 AA.
 DE Human NOVX protein to treat human pathological conditions (SeqID 8).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 26.5%; Score 1067; DB 7; Length 638;
 Best Local Similarity 39.1%; Pred. No. 4.4e-99;
 RESULT 601
 ID ADD18239 standard; protein; 638 AA.
 DE Human molecule (MOL) protein MOL5f.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 26.4%; Score 1066; DB 7; Length 638;
 Best Local Similarity 39.1%; Pred. No. 5.6e-99;
 RESULT 602
 ID ADG76097 standard; protein; 638 AA.
 DE Human NOVX protein to treat human pathological conditions (SeqID 10).
 PN WO2003085096-A2.

PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 26.4%; Score 1066; DB 7; Length 638;
 Best Local Similarity 39.1%; Pred. No. 5.6e-99;
 RESULT 603
 ID AAW17658 standard; protein; 861 AA.
 DE Mouse CD100 antigen.
 PN WO9717368-A1.
 PD 15-MAY-1997.
 PA (DAND) DANA FARBER CANCER INST.
 Query Match 26.4%; Score 1065; DB 2; Length 861;
 Best Local Similarity 39.8%; Pred. No. 1.2e-98;
 RESULT 604
 ID ADP83518 standard; protein; 895 AA.
 DE Breast specific protein of the invention #125.
 PN WO2004052290-A2.
 PD 24-JUN-2004.
 PA (DIAD-) DIADEXUS INC.
 Query Match 26.4%; Score 1064; DB 8; Length 895;
 Best Local Similarity 35.4%; Pred. No. 1.6e-98;
 RESULT 605
 ID AAW58540 standard; protein; 861 AA.
 DE Human semaphorin.
 PN JP10155490-A.
 PD 16-JUN-1998.
 PA (SUMU) SUMITOMO SEIYAKU KK.
 Query Match 26.3%; Score 1062; DB 2; Length 861;
 Best Local Similarity 39.8%; Pred. No. 2.4e-98;
 RESULT 606
 ID AAB51251 standard; protein; 861 AA.
 DE Mouse CD100 protein sequence SEQ ID NO:1.
 PN WO200075655-A1.
 PD 14-DEC-2000.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 26.3%; Score 1062; DB 4; Length 861;
 Best Local Similarity 39.8%; Pred. No. 2.4e-98;
 RESULT 607
 ID AAB81035 standard; protein; 861 AA.
 DE Murine CD100 amino acid sequence.
 PN JP2001048803-A.
 PD 20-FEB-2001.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 26.3%; Score 1062; DB 4; Length 861;
 Best Local Similarity 39.8%; Pred. No. 2.4e-98;
 RESULT 608
 ID ABB98402 standard; protein; 805 AA.
 DE Human NOV2, a semphorin like protein.
 PN WO200255704-A2.
 PD 18-JUL-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 26.2%; Score 1055; DB 5; Length 805;
 Best Local Similarity 36.4%; Pred. No. 1.1e-97;
 RESULT 609
 ID AAW17657 standard; protein; 862 AA.
 DE Human CD100 antigen.
 PN WO9717368-A1.
 PD 15-MAY-1997.

PA (DAND) DANA FARBER CANCER INST.
 Query Match 25.9%; Score 1043; DB 2; Length 862;
 Best Local Similarity 35.2%; Pred. No. 2.1e-96;

RESULT 610
 ID AAB51252 standard; protein; 862 AA.
 DE Human CD100 protein sequence SEQ ID NO:3.
 PN WO200075655-A1.
 PD 14-DEC-2000.

PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 25.9%; Score 1043; DB 4; Length 862;
 Best Local Similarity 35.2%; Pred. No. 2.1e-96;

RESULT 611
 ID AAB81036 standard; protein; 862 AA.
 DE Human CD100 amino acid sequence.
 PN JP2001048803-A.
 PD 20-FEB-2001.

PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 25.9%; Score 1043; DB 4; Length 862;
 Best Local Similarity 35.2%; Pred. No. 2.1e-96;

RESULT 612
 ID ADP23560 standard; protein; 862 AA.
 DE PRO polypeptide SEQ ID NO:738.
 PN WO2004041170-A2.
 PD 21-MAY-2004.

PA (GETH) GENENTECH INC.
 Query Match 25.9%; Score 1043; DB 8; Length 862;
 Best Local Similarity 35.2%; Pred. No. 2.1e-96;

RESULT 613
 ID AAB01396 standard; protein; 681 AA.
 DE Neuron-associated protein.
 PN WO200034477-A2.
 PD 15-JUN-2000.

PA (INCY-) INCYTE PHARM INC.
 Query Match 25.7%; Score 1037.5; DB 3; Length 681;
 Best Local Similarity 39.0%; Pred. No. 5.1e-96;

RESULT 614
 ID AAB48374 standard; protein; 596 AA.
 DE Human SEC7 protein sequence (clone ID 20422974.2).
 PN WO200078802-A2.
 PD 28-DEC-2000.

PA (CURA-) CURAGEN CORP.
 Query Match 25.6%; Score 1032.5; DB 4; Length 596;
 Best Local Similarity 40.2%; Pred. No. 1.3e-95;

RESULT 615
 ID AAB48378 standard; protein; 624 AA.
 DE Human SEC11 protein sequence (clone ID 20422974.0.132-ext2).
 PN WO200078802-A2.
 PD 28-DEC-2000.

PA (CURA-) CURAGEN CORP.
 Query Match 25.6%; Score 1032.5; DB 4; Length 624;
 Best Local Similarity 40.2%; Pred. No. 1.4e-95;

RESULT 616
 ID AAB48373 standard; protein; 590 AA.
 DE Human SEC6 protein sequence (clone ID 20422974.0.132).
 PN WO200078802-A2.
 PD 28-DEC-2000.

PA (CURA-) CURAGEN CORP.

Query Match 25.5%; Score 1028.5; DB 4; Length 590;
 Best Local Similarity 40.2%; Pred. No. 3.4e-95;
 RESULT 617
 ID ABP64686 standard; protein; 675 AA.
 DE Human protein SEQ ID 346.
 PN WO200259260-A2.
 PD 01-AUG-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 25.3%; Score 1020.5; DB 5; Length 675;
 Best Local Similarity 39.6%; Pred. No. 2.8e-94;
 RESULT 618
 ID ADP83519 standard; protein; 626 AA.
 DE Breast specific protein of the invention #126.
 PN WO2004052290-A2.
 PD 24-JUN-2004.
 PA (DIAD-) DIADEXUS INC.
 Query Match 25.3%; Score 1018; DB 8; Length 626;
 Best Local Similarity 41.2%; Pred. No. 4.4e-94;
 RESULT 619
 ID ABM84740 standard; protein; 652 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4989.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 25.0%; Score 1008.5; DB 8; Length 652;
 Best Local Similarity 38.4%; Pred. No. 4.4e-93;
 RESULT 620
 ID ABM84743 standard; protein; 652 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4992.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 25.0%; Score 1008.5; DB 8; Length 652;
 Best Local Similarity 38.4%; Pred. No. 4.4e-93;
 RESULT 621
 ID ABU60951 standard; protein; 785 AA.
 DE Lung specific protein (LSP) #54.
 PN WO200268633-A2.
 PD 06-SEP-2002.
 PA (DIAD-) DIADEXUS INC.
 Query Match 24.1%; Score 972; DB 5; Length 785;
 Best Local Similarity 35.4%; Pred. No. 3.3e-89;
 RESULT 622
 ID ABJ18435 standard; protein; 785 AA.
 DE Breast specific related amino acid sequence SEQ ID No 244.
 PN WO200277232-A2.
 PD 03-OCT-2002.
 PA (DIAD-) DIADEXUS INC.
 Query Match 24.1%; Score 972; DB 6; Length 785;
 Best Local Similarity 35.4%; Pred. No. 3.3e-89;
 RESULT 623
 ID ADR67098 standard; protein; 794 AA.
 DE Human cancer associated protein sequence SEQ ID NO:144.
 PN WO2004074321-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 24.0%; Score 967.5; DB 8; Length 794;

Best Local Similarity 34.6%; Pred. No. 9.7e-89;
 RESULT 624
 ID AAG68304 standard; protein; 865 AA.
 DE Human semaphorin G-like NHP protein SEQ ID NO:33.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 23.8%; Score 961; DB 5; Length 865;
 Best Local Similarity 33.8%; Pred. No. 5.2e-88;
 RESULT 625
 ID AAG68302 standard; protein; 838 AA.
 DE Human semaphorin G-like NHP protein SEQ ID NO:29.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 23.8%; Score 958; DB 5; Length 838;
 Best Local Similarity 34.7%; Pred. No. 1e-87;
 RESULT 626
 ID ABM84741 standard; protein; 623 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4990.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 23.7%; Score 957; DB 8; Length 623;
 Best Local Similarity 38.3%; Pred. No. 7.7e-88;
 RESULT 627
 ID AAG68303 standard; protein; 870 AA.
 DE Human semaphorin G-like NHP protein SEQ ID NO:31.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 23.7%; Score 954.5; DB 5; Length 870;
 Best Local Similarity 33.5%; Pred. No. 2.4e-87;
 RESULT 628
 ID AAG68301 standard; protein; 843 AA.
 DE Human semaphorin G-like NHP protein SEQ ID NO:27.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 23.6%; Score 951.5; DB 5; Length 843;
 Best Local Similarity 34.4%; Pred. No. 4.7e-87;
 RESULT 629
 ID AAB88349 standard; protein; 770 AA.
 DE Human membrane or secretory protein clone PSEC0074.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 22.8%; Score 919.5; DB 4; Length 770;
 Best Local Similarity 32.8%; Pred. No. 7.5e-84;
 RESULT 630
 ID ABM84742 standard; protein; 579 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4991.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 22.6%; Score 910; DB 8; Length 579;
 Best Local Similarity 37.1%; Pred. No. 4.4e-83;

RESULT 631

ID ABM84745 standard; protein; 579 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4994.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 22.6%; Score 910; DB 8; Length 579;
Best Local Similarity 37.1%; Pred. No. 4.4e-83;

RESULT 632

ID AAW51313 standard; protein; 776 AA.
DE Rat semaphorin W.
PN WO9815628-A1.
PD 16-APR-1998.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 22.4%; Score 901.5; DB 2; Length 776;
Best Local Similarity 33.0%; Pred. No. 5.3e-82;

RESULT 633

ID AAY77803 standard; protein; 777 AA.
DE Mouse semaphorin W polypeptide.
PN WO200006725-A1.
PD 10-FEB-2000.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 22.3%; Score 897; DB 3; Length 777;
Best Local Similarity 32.9%; Pred. No. 1.5e-81;

RESULT 634

ID AAG68312 standard; protein; 766 AA.
DE Human semaphorin G-like NHP protein SEQ ID NO:49.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 22.2%; Score 895; DB 5; Length 766;
Best Local Similarity 33.2%; Pred. No. 2.4e-81;

RESULT 635

ID AAG68300 standard; protein; 697 AA.
DE Human semaphorin G-like NHP protein SEQ ID NO:25.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 22.2%; Score 893; DB 5; Length 697;
Best Local Similarity 36.3%; Pred. No. 3.3e-81;

RESULT 636

ID AAG68310 standard; protein; 739 AA.
DE Human semaphorin G-like NHP protein SEQ ID NO:45.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 22.1%; Score 892; DB 5; Length 739;
Best Local Similarity 34.2%; Pred. No. 4.6e-81;

RESULT 637

ID AAG68311 standard; protein; 771 AA.
DE Human semaphorin G-like NHP protein SEQ ID NO:47.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 22.0%; Score 888.5; DB 5; Length 771;
Best Local Similarity 33.0%; Pred. No. 1.1e-80;

RESULT 638

ID AAG68299 standard; protein; 702 AA.
 DE Human semaphorin G-like NHP protein SEQ ID NO:23.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 22.0%; Score 886.5; DB 5; Length 702;
 Best Local Similarity 36.0%; Pred. No. 1.5e-80;
 RESULT 639
 ID AAG68309 standard; protein; 744 AA.
 DE Human semaphorin G-like NHP protein SEQ ID NO:43.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 22.0%; Score 885.5; DB 5; Length 744;
 Best Local Similarity 34.0%; Pred. No. 2.1e-80;
 RESULT 640
 ID ADG76091 standard; protein; 495 AA.
 DE Human NOVX protein to treat human pathological conditions (SeqID 4).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 21.9%; Score 884; DB 7; Length 495;
 Best Local Similarity 41.9%; Pred. No. 1.5e-80;
 RESULT 641
 ID AAM06786 standard; protein; 573 AA.
 DE Human foetal protein, SEQ ID NO: 994.
 PN WO200155339-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 21.3%; Score 859; DB 4; Length 573;
 Best Local Similarity 38.9%; Pred. No. 7.1e-78;
 RESULT 642
 ID ABM84746 standard; protein; 560 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4995.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 21.3%; Score 858.5; DB 8; Length 560;
 Best Local Similarity 35.8%; Pred. No. 7.7e-78;
 RESULT 643
 ID ABM84744 standard; protein; 560 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4993.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 21.3%; Score 858.5; DB 8; Length 560;
 Best Local Similarity 35.8%; Pred. No. 7.7e-78;
 RESULT 644
 ID ABM84747 standard; protein; 560 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4996.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 21.3%; Score 858.5; DB 8; Length 560;
 Best Local Similarity 35.8%; Pred. No. 7.7e-78;
 RESULT 645
 ID ABM84748 standard; protein; 560 AA.

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4997.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 21.3%; Score 858.5; DB 8; Length 560;
Best Local Similarity 35.8%; Pred. No. 7.7e-78;
RESULT 646
ID ABM83768 standard; protein; 754 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4017.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 20.8%; Score 839; DB 8; Length 754;
Best Local Similarity 31.6%; Pred. No. 1.3e-75;
RESULT 647
ID ADL35830 standard; protein; 753 AA.
DE Human semaphorin III family (semaphorin3F) protein.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 20.8%; Score 838.5; DB 8; Length 753;
Best Local Similarity 31.5%; Pred. No. 1.4e-75;
RESULT 648
ID ADI28018 standard; protein; 255 AA.
DE ECMCAD protein 1672338CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 20.7%; Score 835.5; DB 5; Length 255;
Best Local Similarity 70.4%; Pred. No. 4.6e-76;
RESULT 649
ID AAG68308 standard; protein; 598 AA.
DE Human semaphorin G-like NHP protein SEQ ID NO:41.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 20.5%; Score 827; DB 5; Length 598;
Best Local Similarity 35.9%; Pred. No. 1.4e-74;
RESULT 650
ID ADN95333 standard; protein; 770 AA.
DE Human BEC/LEC-related protein sequence SeqID255.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 20.5%; Score 825.5; DB 7; Length 770;
Best Local Similarity 30.5%; Pred. No. 3.1e-74;
RESULT 651
ID AAR71380 standard; protein; 771 AA.
DE Human semaphorin III protein.
PN WO9507706-A1.
PD 23-MAR-1995.
PA (REGC) UNIV CALIFORNIA.
Query Match 20.5%; Score 825.5; DB 2; Length 771;
Best Local Similarity 30.5%; Pred. No. 3.1e-74;
RESULT 652
ID AAG62726 standard; peptide; 771 AA.

DE Amino acid sequence of human semaphorin Sema3A.
PN WO200138491-A2.
PD 31-MAY-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 20.5%; Score 825.5; DB 4; Length 771;
Best Local Similarity 30.5%; Pred. No. 3.1e-74;
RESULT 653
ID ABG96413 standard; protein; 771 AA.
DE Human ovarian cancer marker M473.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 20.5%; Score 825.5; DB 5; Length 771;
Best Local Similarity 30.5%; Pred. No. 3.1e-74;
RESULT 654
ID ADD08934 standard; protein; 771 AA.
DE Human semaphorin 3A protein SEQ ID NO:10.
PN WO2003029814-A2.
PD 10-APR-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 20.5%; Score 825.5; DB 7; Length 771;
Best Local Similarity 30.5%; Pred. No. 3.1e-74;
RESULT 655
ID ADE25760 standard; protein; 771 AA.
DE Human protein differentially expressed in foam cells #37.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 20.5%; Score 825.5; DB 7; Length 771;
Best Local Similarity 30.5%; Pred. No. 3.1e-74;
RESULT 656
ID ADQ19751 standard; protein; 771 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2570.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 20.5%; Score 825.5; DB 8; Length 771;
Best Local Similarity 30.5%; Pred. No. 3.1e-74;
RESULT 657
ID AAG68307 standard; protein; 603 AA.
DE Human semaphorin G-like NHP protein SEQ ID NO:39.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 20.4%; Score 820.5; DB 5; Length 603;
Best Local Similarity 35.6%; Pred. No. 6.7e-74;
RESULT 658
ID AAG62727 standard; peptide; 749 AA.
DE Amino acid sequence of human semaphorin Sema3B.
PN WO200138491-A2.
PD 31-MAY-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 20.3%; Score 820; DB 4; Length 749;
Best Local Similarity 31.2%; Pred. No. 1.1e-73;
RESULT 659
ID ADD08936 standard; protein; 749 AA.

DE Human semaphorin 3B protein SEQ ID NO:12.

PN WO2003029814-A2.

PD 10-APR-2003.

PA (LUDW-) LUDWIG INST CANCER RES.

PA (LICN) LICENTIA LTD.

Query Match 20.3%; Score 820; DB 7; Length 749;

Best Local Similarity 31.2%; Pred. No. 1.1e-73;

RESULT 660

ID ADL82793 standard; protein; 749 AA.

DE Human semaphorin3B, SEMA3B.

PN US2003166557-A1.

PD 04-SEP-2003.

PA (TEXA) UNIV TEXAS SYSTEM.

Query Match 20.3%; Score 820; DB 7; Length 749;

Best Local Similarity 31.2%; Pred. No. 1.1e-73;

RESULT 661

ID ABM80457 standard; protein; 749 AA.

DE Tumour-associated antigenic target (TAT) polypeptide PRO4832, SEQ:1150.

PN WO2004030615-A2.

PD 15-APR-2004.

PA (GETH) GENENTECH INC.

Query Match 20.3%; Score 820; DB 8; Length 749;

Best Local Similarity 31.2%; Pred. No. 1.1e-73;

RESULT 662

ID AAG62731 standard; peptide; 785 AA.

DE Amino acid sequence of human semaphorin Sema3F.

PN WO200138491-A2.

PD 31-MAY-2001.

PA (GEHO) GEN HOSPITAL CORP.

Query Match 20.3%; Score 819.5; DB 4; Length 785;

Best Local Similarity 30.0%; Pred. No. 1.3e-73;

RESULT 663

ID ADD08942 standard; protein; 785 AA.

DE Human semaphorin 3F protein SEQ ID NO:18.

PN WO2003029814-A2.

PD 10-APR-2003.

PA (LUDW-) LUDWIG INST CANCER RES.

PA (LICN) LICENTIA LTD.

Query Match 20.3%; Score 819.5; DB 7; Length 785;

Best Local Similarity 30.0%; Pred. No. 1.3e-73;

RESULT 664

ID AAY21264 standard; protein; 796 AA.

DE Human semaphorin III wild type protein fragment 1.

PN WO9845322-A2.

PD 15-OCT-1998.

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PA (UYUT-) RIJKSUNIV UTRECHT.

Query Match 20.3%; Score 817.5; DB 2; Length 796;

Best Local Similarity 29.9%; Pred. No. 2.2e-73;

RESULT 665

ID ABM83769 standard; protein; 748 AA.

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4018.

PN WO2004023973-A2.

PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.

Query Match 20.1%; Score 811; DB 8; Length 748;

Best Local Similarity 31.1%; Pred. No. 9.1e-73;
 RESULT 666
 ID AAY23873 standard; protein; 737 AA.
 DE SBSEMN1, a semaphorin family polypeptide.
 PN EP933425-A1.
 PD 04-AUG-1999.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Query Match 20.1%; Score 810; DB 2; Length 737;
 Best Local Similarity 30.5%; Pred. No. 1.1e-72;
 RESULT 667
 ID AAY23874 standard; protein; 737 AA.
 DE Protein encoded by an EST sequence encoding SBSEMN1.
 PN EP933425-A1.
 PD 04-AUG-1999.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Query Match 20.0%; Score 805; DB 2; Length 737;
 Best Local Similarity 30.5%; Pred. No. 3.6e-72;
 RESULT 668
 ID AAY99427 standard; protein; 777 AA.
 DE Human PRO1491 (UNQ760) amino acid sequence SEQ ID NO:310.
 PN WO200012708-A2.
 PD 09-MAR-2000.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 3; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 669
 ID AAB66176 standard; protein; 777 AA.
 DE Protein of the invention #88.
 PN WO200078961-A1.
 PD 28-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 4; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 670
 ID AAU29197 standard; protein; 777 AA.
 DE Human PRO polypeptide sequence #174.
 PN WO200168848-A2.
 PD 20-SEP-2001.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 4; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 671
 ID ABU58573 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003027272-A1.
 PD 06-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 672
 ID ABU88121 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003032127-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 673
 ID ABU84436 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 674
ID ABR66310 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 675
ID ABR65700 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 676
ID ABU99640 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 677
ID ABU82879 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 678
ID ABU90000 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 679
ID ABR68249 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 680
ID ABU96302 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 681
ID ABU92733 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.

PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 682
ID ABO08810 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 683
ID ABO02862 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 684
ID ABR75016 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 685
ID ABR94778 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 686
ID ABU85751 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 687
ID ABU98911 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 688
ID ABU98126 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 689
ID ABU91832 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.

PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 690
ID ABU89525 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 691
ID ABU86366 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 692
ID ABU67579 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 693
ID ABU80607 standard; protein; 777 AA.
DE Human PRO protein #174.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 694
ID ABR99525 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 695
ID ABR98915 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 696
ID AB016438 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 697

ID ABR92338 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 698
ID ABO18979 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 699
ID ABR78400 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 700
ID ABU85136 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 701
ID ABO00275 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 702
ID ABO11607 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 703
ID ABO02252 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 704
ID ABU88826 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 705

ID ABU83521 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003036134-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 706
 ID ABO06322 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003022294-A1.
 PD 30-JAN-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 707
 ID ABR59358 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003027275-A1.
 PD 06-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 708
 ID ABO09420 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003027324-A1.
 PD 06-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 709
 ID ABO19284 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003036118-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 710
 ID ABO11302 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003036123-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 711
 ID ABR66920 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003036148-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 712
 ID ABO16133 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003040060-A1.
 PD 27-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 713

ID ABO13839 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003044916-A1.
 PD 06-MAR-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 714
 ID ABU65742 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein, SEQ ID 348.
 PN US2003036156-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 715
 ID ABO07590 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003032117-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 716
 ID ABO03777 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003036128-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 717
 ID ABR67225 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003027266-A1.
 PD 06-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 718
 ID ABO15828 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003054483-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 719
 ID ABU56109 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein, PRO1491.
 PN US2003022298-A1.
 PD 30-JAN-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 720
 ID ABU65437 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003032102-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 721

ID ABU95382 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003036117-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 722
 ID ABU71285 standard; protein; 777 AA.
 DE Human PRO1491 protein.
 PN US2003036143-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 723
 ID ABO07895 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003032130-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 724
 ID ABR70136 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003032138-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 725
 ID ABR69469 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003036132-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 726
 ID ABO01610 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003008353-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 727
 ID ABU81412 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003017542-A1.
 PD 23-JAN-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 728
 ID ABR60209 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003032137-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 729

ID ABR67944 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003027269-A1.

PD 06-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 730

ID ABR65332 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003027268-A1.

PD 06-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 731

ID ABR68554 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003027274-A1.

PD 06-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 732

ID ABR71966 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003032135-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 733

ID ABU85446 standard; protein; 777 AA.

DE Human PRO polypeptide #174.

PN US2003022295-A1.

PD 30-JAN-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 734

ID ABU89136 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003022297-A1.

PD 30-JAN-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 735

ID ABU83216 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003032105-A1.

PD 13-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 736

ID ABU95072 standard; protein; 777 AA.

DE Novel human secreted and transmembrane protein PRO1491.

PN US2003032123-A1.

PD 13-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 737

ID ABU90620 standard; protein; 777 AA.

DE Novel human secreted and transmembrane protein PRO1491.

PN US2003032108-A1.

PD 13-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 738

ID ABU84131 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003032111-A1.

PD 13-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 739

ID ABU93782 standard; protein; 777 AA.

DE Novel human secreted and transmembrane protein PRO1491.

PN US2003032119-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 740

ID ABR65027 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003027263-A1.

PD 06-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 741

ID ABR68859 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003027271-A1.

PD 06-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 742

ID ABO06675 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003036125-A1.

PD 20-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 743

ID ABR99220 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003040068-A1.

PD 27-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 744

ID ABU57104 standard; protein; 777 AA.

DE Human PRO polypeptide #174.

PN US2003027280-A1.

PD 06-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 745

ID ABU86056 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 746

ID ABU82343 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 747

ID ABU87354 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 748

ID ABU83826 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 749

ID ABO08200 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 750

ID ABU81911 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 751

ID ABU66075 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 752

ID ABR59904 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 753

ID ABU94092 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003036155-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 754
 ID ABU99945 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003022296-A1.
 PD 30-JAN-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 755
 ID ABR66615 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003027281-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 756
 ID ABR91033 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003040058-A1.
 PD 27-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 757
 ID ABU94460 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003017540-A1.
 PD 23-JAN-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 758
 ID ABU79342 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003032106-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 759
 ID ABU86671 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003032129-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 760
 ID ABU86976 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003032131-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 761

ID ABU94765 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003032103-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 762
 ID ABO04692 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003032107-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 763
 ID ABR70441 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003032139-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 764
 ID ABU98606 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003022301-A1.
 PD 30-JAN-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 765
 ID ABR66005 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003036165-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 766
 ID ABR64722 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003027262-A1.
 PD 06-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 767
 ID ABU79647 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003032110-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 768
 ID ABU93038 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003036142-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 769

ID ABU95997 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003036145-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 770
 ID ABU91217 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003036154-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 771
 ID ABU90310 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003036153-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 772
 ID ABO09725 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003044931-A1.
 PD 06-MAR-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 773
 ID ABO10997 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003036150-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 774
 ID ABR71051 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003040069-A1.
 PD 27-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 775
 ID ABU87659 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003022293-A1.
 PD 30-JAN-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 776
 ID ABU91527 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003032128-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 777
 ID ABU84741 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 778
ID ABR69831 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 779
ID ABU80208 standard; protein; 777 AA.
DE Human PRO protein #174.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 780
ID ABU93477 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 781
ID ABO10030 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 782
ID ABO09115 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 783
ID ABU10683 standard; protein; 777 AA.
DE Human secreted/transmembrane protein #174.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 784
ID ABU95692 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 785
ID ABU96901 standard; protein; 777 AA.

DE Novel human secreted and transmembrane protein PRO1491.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 786
ID ABR70746 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 787
ID ABO05097 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 788
ID ABO08505 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 789
ID ABO05712 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 790
ID ABR74101 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 791
ID ABR95693 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 792
ID ABR80990 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 793
 ID ABR81295 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003049743-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 794
 ID ABM00991 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003049769-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 795
 ID ABR88593 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068743-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 796
 ID ABM77414 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003054479-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 797
 ID ABO28898 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068685-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 798
 ID ABO31643 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068725-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 799
 ID ABM08060 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068752-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 800

ID ABO40540 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 801

ID ABO35965 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 802

ID ABO44104 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 803

ID ADA78100 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 804

ID ABM24899 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 805

ID ABO03167 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 806

ID ABR90423 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 807

ID ABM17337 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003054459-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 808
ID ABR95083 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 809
ID ABR95388 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 810
ID ABO21626 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 811
ID ABR97890 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 812
ID ABR87678 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 813
ID ABM77719 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 814
ID ABM27949 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 815
ID ABM06230 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 816
ID ABM03736 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 817
ID ABM35187 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 818
ID ABM26424 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 819
ID ABO48206 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 820
ID ABR92948 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 821
ID ABO24709 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 822

ID ABM11720 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 823

ID ABM02821 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 824

ID ABM16117 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 825

ID ABO27678 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 826

ID ABM29169 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 827

ID ABM07145 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 828

ID ABM21239 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 829

ID ABM09585 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003073175-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 830
 ID ABO41455 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068695-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 831
 ID ABO36270 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003068703-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 832
 ID ABO43799 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003068732-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 833
 ID ABM76499 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003082717-A1.
 PD 01-MAY-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 834
 ID ABM76195 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003104548-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 835
 ID ABM25814 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003104542-A1.
 PD 05-JUN-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 836
 ID ABM26119 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003104543-A1.

PD 05-JUN-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 837

ID ABO03472 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003036127-A1.

PD 20-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 838

ID ABO02557 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003040061-A1.

PD 27-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 839

ID ABR90728 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003036130-A1.

PD 20-FEB-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 840

ID ABR73796 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003054468-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 841

ID ABO17048 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003054470-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 842

ID ABR94473 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003044917-A1.

PD 06-MAR-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 843

ID ABR75980 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003044929-A1.

PD 06-MAR-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 844

ID ABR71356 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003059880-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 845
 ID ABR93253 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003064465-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 846
 ID ABR93558 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003054478-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 847
 ID ABR87983 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068718-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 848
 ID ABO33669 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 849
 ID ABO27983 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003064454-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 850
 ID ABO30118 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003064461-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 851
 ID ABO33327 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003068724-A1.

PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 852
 ID ABM05015 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068727-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 853
 ID ABM08975 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068772-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 854
 ID ABO36575 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068714-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 855
 ID ABO35660 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003068758-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 856
 ID ABO39625 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068776-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 857
 ID ABM10500 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003069407-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 858
 ID ABM12025 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003104555-A1.
 PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 859
 ID ABO52171 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003049768-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 860
 ID ABO52476 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003049771-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 861
 ID ABO23794 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003032134-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 862
 ID ABR97280 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003054481-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 863
 ID ABR87068 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003049778-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 864
 ID ABM11110 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003049782-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 865
 ID ABM28254 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003054476-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 866
 ID ABO32253 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068733-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 867
 ID ABM15380 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068692-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 868
 ID ABM06535 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068709-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 869
 ID ABM04346 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068716-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 870
 ID ABM22459 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068740-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 871
 ID ABM07755 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068751-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 872
 ID ABO40845 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068684-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 873

ID ABM35492 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 874

ID ABM33255 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 875

ID ABO52781 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 876

ID ABO50341 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 877

ID ABU99335 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 878

ID ABO04387 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 879

ID ABO06017 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 880

ID ABM18557 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003054480-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 881
ID ABR97585 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 882
ID ABR80685 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 883
ID ABM01296 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 884
ID ABR88898 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 885
ID ABM13550 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 886
ID ABM20934 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 887
ID ABO42065 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 888
 ID ABO42675 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003049751-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 889
 ID ABM10195 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003067478-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 890
 ID ABO38710 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068773-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 891
 ID ABM32950 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003073185-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 892
 ID ABM22764 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003087373-A1.
 PD 08-MAY-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 893
 ID ABM74975 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003096353-A1.
 PD 22-MAY-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 894
 ID ADA79892 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003073173-A1.
 PD 17-APR-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 895
 ID ABR96365 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003054458-A1.

PD 20-MAR-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 896

ID ABM02516 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003059886-A1.

PD 27-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 897

ID ABR86458 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003049758-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 898

ID ABR86763 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003049772-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 899

ID ABM16727 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003064448-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 900

ID ABM29779 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003064456-A1.

PD 03-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 901

ID ABO29203 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003068693-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 902

ID ABM23984 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003068735-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 903
 ID ABM23374 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068753-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 904
 ID ABM22154 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068742-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 905
 ID ABO37795 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068756-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 906
 ID ABM28559 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003082715-A1.
 PD 01-MAY-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 907
 ID ABM28864 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003082716-A1.
 PD 01-MAY-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 908
 ID ABM66508 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068737-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 909
 ID ABM75890 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003104547-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 910

ID ABM34170 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 911

ID ABM34475 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 912

ID ABO20406 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 913

ID ABO21321 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 914

ID ABO22236 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 915

ID ABR96670 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 916

ID ABR85848 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 917

ID ABR99830 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003049763-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 918
 ID ABM00381 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003073172-A1.
 PD 17-APR-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 919
 ID ABM00686 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003073172-A1.
 PD 17-APR-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 920
 ID ABO29813 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068700-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 921
 ID ABM23679 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068736-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 922
 ID ABM29474 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068679-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 923
 ID ABO38405 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068767-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 924
 ID ABO45705 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003073182-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 925
 ID ABM20629 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003104557-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 926
 ID ADA81619 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003092121-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 927
 ID ABO16743 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003027276-A1.
 PD 06-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 928
 ID ABO18369 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003044920-A1.
 PD 06-MAR-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 929
 ID ABO22796 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003027265-A1.
 PD 06-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 930
 ID ABO23101 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003054461-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 931
 ID ABR92643 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003064446-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 932
 ID ABR81600 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003049744-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 933
 ID ABM78024 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003049783-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 934
 ID ABR89813 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003073171-A1.
 PD 17-APR-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 935
 ID ABM26729 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003032121-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 936
 ID ABM13855 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003064458-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 937
 ID ABO28593 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003064460-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 938
 ID ABO30423 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003064464-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 939
 ID ABM07450 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068702-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 940

ID ABM04041 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003068734-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 941

ID ABO37185 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003068719-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 942

ID ABO41760 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003068729-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 943

ID ABO35355 standard; protein; 777 AA.

DE Human PRO polypeptide #174.

PN US2003068738-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 944

ID ABM25204 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003104540-A1.

PD 05-JUN-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 945

ID ABO47596 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003049742-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 946

ID ABO47901 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003049747-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 947
 ID ABO48511 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003049750-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 948
 ID ABO51561 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003049766-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 949
 ID ABO51866 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003049767-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 950
 ID ABO50646 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003049779-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 951
 ID ABR79770 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003040059-A1.
 PD 27-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 952
 ID ABM17032 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003040078-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 953
 ID ABO18064 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003044918-A1.
 PD 06-MAR-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 954
 ID ABO21016 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 955
ID ABR96975 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 956
ID ABM12330 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 957
ID ABM16422 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 958
ID ABM24289 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 959
ID ABM14770 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 960
ID ABM04651 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 961
ID ABM06840 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068730-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 962

ID ABM09280 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003073174-A1.

PD 17-APR-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 963

ID ABO39320 standard; protein; 777 AA.

DE Human secreted/transmembrane protein (PRO) #174.

PN US2003068775-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 964

ID ABM75585 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003104545-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 965

ID ABM25509 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003104541-A1.

PD 05-JUN-2003.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 966

ID ABM20019 standard; protein; 777 AA.

DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003104554-A1.

PD 05-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 967

ID ABO46925 standard; protein; 777 AA.

DE Human PRO polypeptide #174.

PN US2003049762-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 968

ID ABO47230 standard; protein; 777 AA.

DE Human PRO polypeptide #174.

PN US2003049765-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 969

ID ADA83417 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 970

ID ABR71661 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 971

ID ABR72271 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 972

ID ABR98610 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 973

ID ABO06980 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 974

ID ABR84933 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 975

ID ABR73491 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 976

ID ABR76585 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 977
 ID ABR73186 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003027270-A1.
 PD 06-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 978
 ID ABM18252 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003054469-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 979
 ID ABO20711 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003032126-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 980
 ID ABO25454 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003054463-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 981
 ID ABO25759 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003054466-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 982
 ID ABR94168 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003059879-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 983
 ID ABR80075 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003049738-A1.
 PD 13-MAR-2003.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 984
 ID ABM11415 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003064469-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 985
 ID ABO33022 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003064453-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 986
 ID ABO30728 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003064466-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 987
 ID ABO31033 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003064468-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 988
 ID ABM27339 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068760-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 989
 ID ABM30084 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068769-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 990
 ID ABM05620 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003045700-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 991
 ID ABM15685 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068698-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 992
ID ABM08670 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 993
ID ABO42370 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 994
ID ABO38100 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 995
ID ABO46010 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 996
ID ABM66813 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 997
ID ADB20460 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 19.7%; Score 793.5; DB 6; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 998
ID ABM19714 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 999
 ID ABO49426 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003049774-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1000
 ID ABO49731 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003049775-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1001
 ID ADA78712 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003073181-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1002
 ID ABR88288 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068720-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1003
 ID ABM27034 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068739-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1004
 ID ABM03431 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068763-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1005
 ID ABO39930 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068689-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 6; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1006
 ID ABO50036 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003049776-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1007
 ID ABO50951 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003049780-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1008
 ID ABO05407 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003036126-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1009
 ID ABR74711 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003044924-A1.
 PD 06-MAR-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1010
 ID ABO44522 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1011
 ID ABR77190 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003044927-A1.
 PD 06-MAR-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1012
 ID ABM17947 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003040072-A1.
 PD 27-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1013
 ID ABR95998 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003040073-A1.

PD 27-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1014
 ID ABO21931 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003054475-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1015
 ID ABO20101 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003032124-A1.
 PD 13-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1016
 ID ABO24404 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003064467-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1017
 ID ABR86153 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003049759-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1018
 ID ABM10805 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003064455-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1019
 ID ABM76804 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003054465-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1020
 ID ABR89508 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003073170-A1.
 PD 17-APR-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1021

ID ABM12635 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1022

ID ABM05925 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1023

ID ABO35050 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1024

ID ABM03126 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1025

ID ABM19104 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1026

ID ABM19409 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1027

ID ABO46620 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1028

ID ABO49121 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003049757-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1029
 ID ABR69164 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003027273-A1.
 PD 06-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1030
 ID ABR89203 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003036119-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1031
 ID ABR72576 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003036120-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1032
 ID ABR74406 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003036161-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1033
 ID ABO18674 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003044921-A1.
 PD 06-MAR-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1034
 ID ABR80380 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003049739-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1035
 ID ABM01601 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003059882-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1036
 ID ABM02211 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003059884-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1037
 ID ABR87373 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068687-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1038
 ID ABM12940 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003073186-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1039
 ID ABM30694 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003064443-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1040
 ID ABM24594 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003064444-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1041
 ID ABO29508 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068697-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1042
 ID ABO31338 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068710-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1043
 ID ABM14465 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068686-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1044
 ID ABM09890 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003073178-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1045
 ID ABO39015 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003068774-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1046
 ID ABM34780 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003104538-A1.
 PD 05-JUN-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1047
 ID ABO51256 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003049781-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1048
 ID ABO04082 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003036158-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1049
 ID ABO10552 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003036151-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1050
 ID ABR77795 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003040067-A1.
 PD 27-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1051
 ID ABR79005 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003054456-A1.
 PD 20-MAR-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1052
 ID ABO24099 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003054482-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1053
 ID ABR93863 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003054457-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1054
 ID ABM01906 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003059883-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1055
 ID ABM78329 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003049764-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1056
 ID ABO33546 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1057
 ID ABR90118 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003073177-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1058

ID ABM27644 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1059

ID ABM13245 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1060

ID ABO31948 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1061

ID ABM14160 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068683-A1.
PD 10-APR-2003.

Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1062

ID ABM08365 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1063

ID ABO40235 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003068681-A1.
PD 10-APR-2003.

Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1064

ID ABM74670 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1065

ID ABM33865 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003096358-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1066
 ID ABM20324 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003104556-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1067
 ID ABO48816 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003049756-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1068
 ID ABR72881 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003036122-A1.
 PD 20-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1069
 ID ABO15523 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003036121-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1070
 ID ABR85238 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003040065-A1.
 PD 27-FEB-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1071
 ID ABO15218 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003044919-A1.
 PD 06-MAR-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1072
 ID ABO17353 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003040077-A1.
 PD 27-FEB-2003.

Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1073
 ID ABM17642 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003044928-A1.
 PD 06-MAR-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1074
 ID ABR85543 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003049746-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1075
 ID ABM77109 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003054464-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1076
 ID ABO28288 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003064459-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1077
 ID ABM23069 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068757-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1078
 ID ABM30389 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068723-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1079
 ID ABM21849 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068741-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1080

ID ABM21544 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1081

ID ABM15075 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1082

ID ABO41150 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1083

ID ABO36880 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1084

ID ABO37490 standard; protein; 777 AA.
DE Human secreted/transmembrane protein (PRO) #174.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1085

ID ABM75280 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1086

ID ABM33560 standard; protein; 777 AA.
DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;

RESULT 1087

ID ABO46315 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003049760-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1088
 ID ADA82783 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003049755-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1089
 ID ABM31914 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068680-A1.
 PD 10-APR-2003.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1090
 ID ABM31304 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068762-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1091
 ID ADB86091 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003054472-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1092
 ID ABM32219 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068708-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1093
 ID ABM32524 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068713-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1094
 ID ABM31609 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.

PN US2003068761-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1095
 ID ABM30999 standard; protein; 777 AA.
 DE Human secreted polypeptide PRO1491, SEQ ID NO:348.
 PN US2003068771-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1096
 ID ADC18179 standard; protein; 777 AA.
 DE Human PRO polypeptide #88.
 PN US2003064925-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1097
 ID ADD05821 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003087376-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1098
 ID ADD70825 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003099625-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1099
 ID ADD39902 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003083462-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1100
 ID ADD70348 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003054406-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1101
 ID ADD38469 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003096955-A1.

PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1102
 ID ADD39425 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003096954-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1103
 ID ADD38948 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003092061-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1104
 ID ADD40379 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003082627-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1105
 ID ADE50600 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003069179-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1106
 ID ADE20212 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003092883-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1107
 ID ADE50123 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003082626-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1108
 ID ADE21681 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003082628-A1.
 PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1109
ID ADF30106 standard; protein; 777 AA.
DE Human secreted/transmembrane protein PRO1491.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1110
ID ADF55999 standard; protein; 777 AA.
DE Human secreted/transmembrane protein PRO1491.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1111
ID ADG02816 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1112
ID ADG01523 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1113
ID ADF95698 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1114
ID ADG12513 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 19.7%; Score 793.5; DB 7; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1115
ID ADH09173 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 7; Length 777;

Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1116
 ID ADH99503 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003065142-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1117
 ID ADL32954 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003207396-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1118
 ID ADM30488 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003073813-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 7; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1119
 ID ADE74485 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003211572-A1.
 PD 13-NOV-2003.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1120
 ID ADE75097 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein (PRO) #174.
 PN US2003211574-A1.
 PD 13-NOV-2003.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1121
 ID ADE96683 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003195347-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1122
 ID ADF25994 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003199675-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1123
 ID ADF24893 standard; protein; 777 AA.

DE Human secreted/transmembrane protein PRO1491.
 PN US2003198993-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1124
 ID ADF29629 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003203401-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1125
 ID ADE97160 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003195334-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1126
 ID ADF96310 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003215909-A1.
 PD 20-NOV-2003.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1127
 ID ADG04581 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003215912-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1128
 ID ADG00741 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003215911-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1129
 ID ADG82997 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003215910-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1130
 ID ADH03198 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003216562-A1.

PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1131
 ID ADH04152 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003220471-A1.
 PD 27-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1132
 ID ADH03675 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2003224478-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1133
 ID ADH26278 standard; protein; 777 AA.
 DE Novel human secreted and transmembrane protein PRO1491.
 PN US2003068770-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1134
 ID ADH33247 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2003068768-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1135
 ID ADH04629 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2004005626-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1136
 ID ADH61630 standard; protein; 777 AA.
 DE Human secreted/transmembrane protein PRO1491.
 PN US2004014130-A1.
 PD 22-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 19.7%; Score 793.5; DB 8; Length 777;
 Best Local Similarity 31.0%; Pred. No. 6e-71;
 RESULT 1137
 ID ADJ54986 standard; protein; 777 AA.
 DE Human PRO polypeptide #174.
 PN US2004023321-A1.
 PD 05-FEB-2004.

PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 8; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1138
ID ADJ64757 standard; protein; 777 AA.
DE Human PRO polypeptide #174.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 8; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1139
ID ADM31653 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 8; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1140
ID ADM36700 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 8; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1141
ID ADM40505 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 8; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1142
ID ADL94829 standard; protein; 777 AA.
DE Human secreted/transmembrane protein PRO1491.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 8; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1143
ID ADN38113 standard; protein; 777 AA.
DE Novel human secreted and transmembrane protein PRO1491.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 19.7%; Score 793.5; DB 8; Length 777;
Best Local Similarity 31.0%; Pred. No. 6e-71;
RESULT 1144
ID AAY27127 standard; protein; 777 AA.
DE Human brain tissue-derived polypeptide (clone OM007).
PN WO9933873-A1.
PD 08-JUL-1999.
PA (ONOH) ONO PHARM CO LTD.

Query Match 19.7%; Score 792.5; DB 2; Length 777;
 Best Local Similarity 31.0%; Pred. No. 7.6e-71;
 RESULT 1145
 ID AAW30617 standard; protein; 751 AA.
 DE Human semaphorin E protein from clone BR5334.
 PN WO9853065-A1.
 PD 26-NOV-1998.
 PA (GEMY) GENETICS INST INC.
 Query Match 19.4%; Score 782.5; DB 2; Length 751;
 Best Local Similarity 30.6%; Pred. No. 7.6e-70;
 RESULT 1146
 ID AAB28379 standard; protein; 751 AA.
 DE Clone BR533_4.
 PN WO200063692-A1.
 PD 26-OCT-2000.
 PA (GEMY) GENETICS INST INC.
 Query Match 19.4%; Score 782.5; DB 3; Length 751;
 Best Local Similarity 30.6%; Pred. No. 7.6e-70;
 RESULT 1147
 ID AAG62728 standard; peptide; 751 AA.
 DE Amino acid sequence of human semaphorin Sema3C.
 PN WO200138491-A2.
 PD 31-MAY-2001.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match 19.4%; Score 782.5; DB 4; Length 751;
 Best Local Similarity 30.6%; Pred. No. 7.6e-70;
 RESULT 1148
 ID ABP68623 standard; protein; 751 AA.
 DE Human pancreatic cancer expressed protein SEQ ID NO 172.
 PN WO200260317-A2.
 PD 08-AUG-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 19.4%; Score 782.5; DB 5; Length 751;
 Best Local Similarity 30.6%; Pred. No. 7.6e-70;
 RESULT 1149
 ID ABU89764 standard; protein; 751 AA.
 DE Protein differentially expressed in cardiovascular disease #58.
 PN WO2003031650-A2.
 PD 17-APR-2003.
 PA (FARB) BAYER AG.
 Query Match 19.4%; Score 782.5; DB 6; Length 751;
 Best Local Similarity 30.6%; Pred. No. 7.6e-70;
 RESULT 1150
 ID ADB75535 standard; protein; 751 AA.
 DE Prostate cancer marker protein.
 PN WO2003009814-A2.
 PD 06-FEB-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 19.4%; Score 782.5; DB 7; Length 751;
 Best Local Similarity 30.6%; Pred. No. 7.6e-70;
 RESULT 1151
 ID ADC38856 standard; protein; 751 AA.
 DE Human secreted protein #100.
 PN US2002193567-A1.
 PD 19-DEC-2002.
 PA (GEMY) GENETICS INST INC.
 Query Match 19.4%; Score 782.5; DB 7; Length 751;

Best Local Similarity 30.6%; Pred. No. 7.6e-70;
 RESULT 1152
 ID ADD08938 standard; protein; 751 AA.
 DE Human semaphorin 3C protein SEQ ID NO:14.
 PN WO2003029814-A2.
 PD 10-APR-2003.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 Query Match 19.4%; Score 782.5; DB 7; Length 751;
 Best Local Similarity 30.6%; Pred. No. 7.6e-70;
 RESULT 1153
 ID ADQ19446 standard; protein; 751 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2265.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 19.4%; Score 782.5; DB 8; Length 751;
 Best Local Similarity 30.6%; Pred. No. 7.6e-70;
 RESULT 1154
 ID ADP23608 standard; protein; 751 AA.
 DE PRO polypeptide SEQ ID NO:786.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 19.4%; Score 782.5; DB 8; Length 751;
 Best Local Similarity 30.6%; Pred. No. 7.6e-70;
 RESULT 1155
 ID ADM72136 standard; protein; 667 AA.
 DE Human NTRAN polypeptide (clone ID 7523644CD1).
 PN WO2004022705-A2.
 PD 18-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 19.1%; Score 770; DB 8; Length 667;
 Best Local Similarity 32.5%; Pred. No. 1.2e-68;
 RESULT 1156
 ID AAG62729 standard; peptide; 807 AA.
 DE Amino acid sequence of human semaphorin Sema3D.
 PN WO200138491-A2.
 PD 31-MAY-2001.
 PA (GEHO) GEN HOSPITAL CORP.
 Query Match 18.7%; Score 755.5; DB 4; Length 807;
 Best Local Similarity 29.5%; Pred. No. 4.9e-67;
 RESULT 1157
 ID ADJ70197 standard; protein; 636 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID2003.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 18.3%; Score 738.5; DB 7; Length 636;
 Best Local Similarity 32.2%; Pred. No. 1.8e-65;
 RESULT 1158
 ID AAB23609 standard; protein; 782 AA.
 DE Human secreted protein SEQ ID NO: 18.
 PN WO200049134-A1.
 PD 24-AUG-2000.
 PA (ALPH-) ALPHAGENE INC.

Query Match 18.3%; Score 737; DB 3; Length 782;
 Best Local Similarity 28.9%; Pred. No. 3.7e-65;
 RESULT 1159
 ID AAG65620 standard; protein; 782 AA.
 DE Novel human protein (NHP) sequence.
 PN WO200170806-A2.
 PD 27-SEP-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 18.3%; Score 737; DB 4; Length 782;
 Best Local Similarity 28.9%; Pred. No. 3.7e-65;
 RESULT 1160
 ID ADJ34115 standard; protein; 782 AA.
 DE Human secreted protein NOV1b.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 18.3%; Score 737; DB 8; Length 782;
 Best Local Similarity 28.9%; Pred. No. 3.7e-65;
 RESULT 1161
 ID ADN04922 standard; protein; 782 AA.
 DE Antipsoriatic protein sequence #641.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 18.3%; Score 737; DB 8; Length 782;
 Best Local Similarity 28.9%; Pred. No. 3.7e-65;
 RESULT 1162
 ID ADQ20125 standard; protein; 782 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2945.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 18.3%; Score 737; DB 8; Length 782;
 Best Local Similarity 28.9%; Pred. No. 3.7e-65;
 RESULT 1163
 ID AAG65619 standard; protein; 875 AA.
 DE Novel human protein (NHP) sequence.
 PN WO200170806-A2.
 PD 27-SEP-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 18.3%; Score 737; DB 4; Length 875;
 Best Local Similarity 28.7%; Pred. No. 4.4e-65;
 RESULT 1164
 ID ADJ34113 standard; protein; 800 AA.
 DE Human secreted protein NOV1a.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 18.1%; Score 730; DB 8; Length 800;
 Best Local Similarity 28.3%; Pred. No. 2e-64;
 RESULT 1165
 ID ADE08371 standard; protein; 1127 AA.
 DE Novel protein (useful for identifying genetic disorders) #526.
 PN WO2003054152-A2.
 PD 03-JUL-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 18.1%; Score 728; DB 7; Length 1127;

Best Local Similarity 33.2%; Pred. No. 5.7e-64;
 RESULT 1166
 ID AAB23636 standard; protein; 785 AA.
 DE Human secreted protein SEQ ID NO: 92.
 PN WO200049134-A1.
 PD 24-AUG-2000.
 PA (ALPH-) ALPHAGENE INC.
 Query Match 18.0%; Score 725.5; DB 3; Length 785;
 Best Local Similarity 28.8%; Pred. No. 5.5e-64;
 RESULT 1167
 ID ADS73261 standard; protein; 1093 AA.
 DE Human kidney tumour specific cDNA K1622P, protein from ORF #3.
 PN US2003109434-A1.
 PD 12-JUN-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 17.9%; Score 723.5; DB 5; Length 1093;
 Best Local Similarity 34.6%; Pred. No. 1.5e-63;
 RESULT 1168
 ID ADD18220 standard; protein; 1093 AA.
 DE Human molecule (MOL) protein MOL4b.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 17.9%; Score 723.5; DB 7; Length 1093;
 Best Local Similarity 34.6%; Pred. No. 1.5e-63;
 RESULT 1169
 ID ADJ34129 standard; protein; 1093 AA.
 DE Human secreted protein NOV2g.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 17.9%; Score 723.5; DB 8; Length 1093;
 Best Local Similarity 34.6%; Pred. No. 1.5e-63;
 RESULT 1170
 ID ADF72704 standard; protein; 1095 AA.
 DE Human cancer-related gene protein sequence SEQ ID NO:34.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 17.9%; Score 723.5; DB 8; Length 1095;
 Best Local Similarity 34.6%; Pred. No. 1.6e-63;
 RESULT 1171
 ID ADF72678 standard; protein; 1095 AA.
 DE Human cancer-related gene protein sequence SEQ ID NO:8.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 17.9%; Score 723.5; DB 8; Length 1095;
 Best Local Similarity 34.6%; Pred. No. 1.6e-63;
 RESULT 1172
 ID ADF72691 standard; protein; 1095 AA.
 DE Human cancer-related gene protein sequence SEQ ID NO:21.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 17.9%; Score 723.5; DB 8; Length 1095;
 Best Local Similarity 34.6%; Pred. No. 1.6e-63;

RESULT 1173

ID ADD18222 standard; protein; 1130 AA.

DE Human molecule (MOL) protein MOL4c.

PN WO2003003984-A2.

PD 16-JAN-2003.

PA (CURA-) CURAGEN CORP.

Query Match 17.9%; Score 723.5; DB 7; Length 1130;

Best Local Similarity 34.6%; Pred. No. 1.6e-63;

RESULT 1174

ID ADJ34119 standard; protein; 1130 AA.

DE Human secreted protein NOV2b.

PN WO2004000997-A2.

PD 31-DEC-2003.

PA (CURA-) CURAGEN CORP.

Query Match 17.9%; Score 723.5; DB 8; Length 1130;

Best Local Similarity 34.6%; Pred. No. 1.6e-63;

RESULT 1175

ID ADF72693 standard; protein; 1150 AA.

DE Human cancer-related gene protein sequence SEQ ID NO:23.

PN WO2003101400-A2.

PD 11-DEC-2003.

PA (AVAL-) AVALON PHARM INC.

Query Match 17.9%; Score 723.5; DB 8; Length 1150;

Best Local Similarity 34.6%; Pred. No. 1.7e-63;

RESULT 1176

ID ADF72706 standard; protein; 1150 AA.

DE Human cancer-related gene protein sequence SEQ ID NO:36.

PN WO2003101400-A2.

PD 11-DEC-2003.

PA (AVAL-) AVALON PHARM INC.

Query Match 17.9%; Score 723.5; DB 8; Length 1150;

Best Local Similarity 34.6%; Pred. No. 1.7e-63;

RESULT 1177

ID ADF72680 standard; protein; 1150 AA.

DE Human cancer-related gene protein sequence SEQ ID NO:10.

PN WO2003101400-A2.

PD 11-DEC-2003.

PA (AVAL-) AVALON PHARM INC.

Query Match 17.9%; Score 723.5; DB 8; Length 1150;

Best Local Similarity 34.6%; Pred. No. 1.7e-63;

RESULT 1178

ID ADS73260 standard; protein; 1151 AA.

DE Human kidney tumour specific cDNA K1622P, protein from ORF #2.

PN US2003109434-A1.

PD 12-JUN-2003.

PA (CORI-) CORIXA CORP.

Query Match 17.9%; Score 723.5; DB 5; Length 1151;

Best Local Similarity 34.6%; Pred. No. 1.7e-63;

RESULT 1179

ID ADS73259 standard; protein; 1202 AA.

DE Human kidney tumour specific cDNA K1622P, protein from ORF #1.

PN US2003109434-A1.

PD 12-JUN-2003.

PA (CORI-) CORIXA CORP.

Query Match 17.9%; Score 723.5; DB 5; Length 1202;

Best Local Similarity 34.6%; Pred. No. 1.8e-63;

RESULT 1180

ID ADF72695 standard; protein; 1203 AA.
DE Human cancer-related gene protein sequence SEQ ID NO:25.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 17.9%; Score 723.5; DB 8; Length 1203;
Best Local Similarity 34.6%; Pred. No. 1.8e-63;
RESULT 1181
ID ADF72682 standard; protein; 1203 AA.
DE Human cancer-related gene protein sequence SEQ ID NO:12.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 17.9%; Score 723.5; DB 8; Length 1203;
Best Local Similarity 34.6%; Pred. No. 1.8e-63;
RESULT 1182
ID ADF72708 standard; protein; 1203 AA.
DE Human cancer-related gene protein sequence SEQ ID NO:38.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 17.9%; Score 723.5; DB 8; Length 1203;
Best Local Similarity 34.6%; Pred. No. 1.8e-63;
RESULT 1183
ID ADF72694 standard; protein; 1211 AA.
DE Human cancer-related gene protein sequence SEQ ID NO:24.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 17.9%; Score 723.5; DB 8; Length 1211;
Best Local Similarity 34.6%; Pred. No. 1.8e-63;
RESULT 1184
ID ADF72707 standard; protein; 1211 AA.
DE Human cancer-related gene protein sequence SEQ ID NO:37.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 17.9%; Score 723.5; DB 8; Length 1211;
Best Local Similarity 34.6%; Pred. No. 1.8e-63;
RESULT 1185
ID ADF72681 standard; protein; 1211 AA.
DE Human cancer-related gene protein sequence SEQ ID NO:11.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 17.9%; Score 723.5; DB 8; Length 1211;
Best Local Similarity 34.6%; Pred. No. 1.8e-63;
RESULT 1186
ID ADF72696 standard; protein; 1240 AA.
DE Human cancer-related gene protein sequence SEQ ID NO:26.
PN WO2003101400-A2.
PD 11-DEC-2003.
PA (AVAL-) AVALON PHARM INC.
Query Match 17.9%; Score 723.5; DB 8; Length 1240;
Best Local Similarity 34.6%; Pred. No. 1.9e-63;
RESULT 1187
ID ADF72709 standard; protein; 1240 AA.

DE Human cancer-related gene protein sequence SEQ ID NO:39.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 17.9%; Score 723.5; DB 8; Length 1240;
 Best Local Similarity 34.6%; Pred. No. 1.9e-63;
 RESULT 1188
 ID ADF72683 standard; protein; 1240 AA.
 DE Human cancer-related gene protein sequence SEQ ID NO:13.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 17.9%; Score 723.5; DB 8; Length 1240;
 Best Local Similarity 34.6%; Pred. No. 1.9e-63;
 RESULT 1189
 ID ADF72692 standard; protein; 1248 AA.
 DE Human cancer-related gene protein sequence SEQ ID NO:22.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 17.9%; Score 723.5; DB 8; Length 1248;
 Best Local Similarity 34.6%; Pred. No. 1.9e-63;
 RESULT 1190
 ID ADF72705 standard; protein; 1248 AA.
 DE Human cancer-related gene protein sequence SEQ ID NO:35.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 17.9%; Score 723.5; DB 8; Length 1248;
 Best Local Similarity 34.6%; Pred. No. 1.9e-63;
 RESULT 1191
 ID ADF72679 standard; protein; 1248 AA.
 DE Human cancer-related gene protein sequence SEQ ID NO:9.
 PN WO2003101400-A2.
 PD 11-DEC-2003.
 PA (AVAL-) AVALON PHARM INC.
 Query Match 17.9%; Score 723.5; DB 8; Length 1248;
 Best Local Similarity 34.6%; Pred. No. 1.9e-63;
 RESULT 1192
 ID AAE18212 standard; protein; 1352 AA.
 DE Human MOL4 protein.
 PN WO200206339-A2.
 PD 24-JAN-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 17.9%; Score 723.5; DB 5; Length 1352;
 Best Local Similarity 34.6%; Pred. No. 2.2e-63;
 RESULT 1193
 ID ADD18202 standard; protein; 1352 AA.
 DE Human molecule (MOL) protein MOL4a.
 PN WO2003003984-A2.
 PD 16-JAN-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 17.9%; Score 723.5; DB 7; Length 1352;
 Best Local Similarity 34.6%; Pred. No. 2.2e-63;
 RESULT 1194
 ID ADJ34117 standard; protein; 1352 AA.
 DE Human secreted protein NOV2a.

PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 17.9%; Score 723.5; DB 8; Length 1352;
 Best Local Similarity 34.6%; Pred. No. 2.2e-63;
 RESULT 1195
 ID ADJ34133 standard; protein; 1352 AA.
 DE Human secreted protein NOV2i.
 PN WO2004000997-A2.
 PD 31-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 17.9%; Score 723.5; DB 8; Length 1352;
 Best Local Similarity 34.6%; Pred. No. 2.2e-63;
 RESULT 1196
 ID AAG68291 standard; protein; 1034 AA.
 DE Human semaphorin G-like NHP protein SEQ ID NO:6.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 17.9%; Score 721.5; DB 5; Length 1034;
 Best Local Similarity 34.6%; Pred. No. 2.3e-63;
 RESULT 1197
 ID AAG68289 standard; protein; 1049 AA.
 DE Human semaphorin G-like NHP protein SEQ ID NO:2.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 17.9%; Score 721.5; DB 5; Length 1049;
 Best Local Similarity 34.6%; Pred. No. 2.3e-63;
 RESULT 1198
 ID AAG68292 standard; protein; 1078 AA.
 DE Human semaphorin G-like NHP protein SEQ ID NO:8.
 PN WO200188133-A2.
 PD 22-NOV-2001.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 17.9%; Score 721.5; DB 5; Length 1078;
 Best Local Similarity 34.6%; Pred. No. 2.4e-63;
 RESULT 1199
 ID ABG34077 standard; protein; 1092 AA.
 DE Human Pro peptide #48.
 PN WO200224888-A2.
 PD 28-MAR-2002.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 5; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1200
 ID ADA01364 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003068779-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 6; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1201
 ID ADA43793 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003064474-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 6; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1202
ID ADA43561 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 6; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1203
ID ADA01236 standard; protein; 1092 AA.
DE Human PRO polypeptide #48.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 6; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1204
ID ADA01120 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 7; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1205
ID ADA43677 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 7; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1206
ID ADA06939 standard; protein; 1092 AA.
DE Human PRO polypeptide #48.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 7; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1207
ID ADA08427 standard; protein; 1092 AA.
DE Novel human secreted and transmembrane protein PRO34001.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 7; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1208
ID ADB99720 standard; protein; 1092 AA.
DE Human PRO polypeptide SEQ ID 96.
PN US2003082728-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 7; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1209

ID ADB87003 standard; protein; 1092 AA.

DE Human PRO polypeptide #48.

PN US2003082726-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 7; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1210

ID ADB66158 standard; protein; 1092 AA.

DE Human secreted/transmembrane polypeptide PRO34001.

PN US2003082729-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 7; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1211

ID ADB99836 standard; protein; 1092 AA.

DE Human PRO polypeptide SEQ ID 96.

PN US2003073192-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 7; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1212

ID ADB99491 standard; protein; 1092 AA.

DE Novel human secreted and transmembrane protein PRO34001.

PN US2003082731-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 7; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1213

ID ADB66042 standard; protein; 1092 AA.

DE Human secreted/transmembrane polypeptide PRO34001.

PN US2003082732-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 7; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1214

ID ADC23440 standard; protein; 1092 AA.

DE Human transmembrane PRO polypeptide (SeqID 96).

PN US2003073193-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 7; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1215

ID ADC26133 standard; protein; 1092 AA.

DE Human PRO34001 protein.

PN US2003073194-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1216
 ID ADE04960 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003068778-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1217
 ID ADE11266 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003073191-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1218
 ID ADD88197 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003082733-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1219
 ID ADD95492 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003064473-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1220
 ID ADE06422 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003073195-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1221
 ID ADE38197 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003119120-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1222
 ID ADD88313 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003073189-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1223
 ID ADD90894 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003073188-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1224
 ID ADF99449 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003078401-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1225
 ID ADG06542 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003077742-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1226
 ID ADG05493 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003077741-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1227
 ID ADG82494 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003077744-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 7; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1228
 ID ADE51747 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003104560-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1229
 ID ADE51863 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003104561-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1230

ID ADE37721 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1231

ID ADE37605 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1232

ID ADD95376 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1233

ID ADE38076 standard; protein; 1092 AA.
DE Human PRO polypeptide #48.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1234

ID ADE76165 standard; protein; 1092 AA.
DE Human PRO polypeptide #48.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1235

ID ADE39488 standard; protein; 1092 AA.
DE Human PRO polypeptide #48.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1236

ID ADE04292 standard; protein; 1092 AA.
DE Human PRO polypeptide #48.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1237

ID ADE39889 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003138896-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1238
 ID ADE19754 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003138903-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1239
 ID ADE77332 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003124666-A1.
 PD 03-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1240
 ID ADE65440 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003119116-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1241
 ID ADE76049 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003124663-A1.
 PD 03-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1242
 ID ADE37960 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003119119-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1243
 ID ADE64570 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003119114-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1244
 ID ADE38905 standard; protein; 1092 AA.

DE Human PRO polypeptide #48.
 PN US2003096363-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1245
 ID ADE51979 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003104562-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1246
 ID ADD91010 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003138902-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1247
 ID ADE38789 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003108996-A1.
 PD 12-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1248
 ID ADE37489 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003104563-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1249
 ID ADE06305 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003138898-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1250
 ID ADD90165 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003138904-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1251
 ID ADE38673 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.

PN US2003119086-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1252
 ID ADE39604 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003119118-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1253
 ID ADD89209 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003138897-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1254
 ID ADD88976 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003138899-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1255
 ID ADE19870 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003138900-A1.
 PD 24-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1256
 ID ADE77448 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003124667-A1.
 PD 03-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1257
 ID ADE65324 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003119113-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;
 RESULT 1258
 ID ADE39372 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003119115-A1.

PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1259
ID ADE38557 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1260
ID ADG11110 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1261
ID ADG10994 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1262
ID ADH31522 standard; protein; 1092 AA.
DE Human PRO polypeptide #48.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1263
ID ADH38770 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1264
ID ADH29405 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;
RESULT 1265
ID ADH23708 standard; protein; 1092 AA.
DE Human secreted/transmembrane polypeptide PRO34001.
PN US2003119143-A1.
PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1266

ID ADH27038 standard; protein; 1092 AA.

DE Human secreted/transmembrane polypeptide PRO34001.

PN US2003119135-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1267

ID ADH38306 standard; protein; 1092 AA.

DE Novel human secreted and transmembrane protein PRO34001.

PN US2003119124-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1268

ID ADH26922 standard; protein; 1092 AA.

DE Human secreted/transmembrane polypeptide PRO34001.

PN US2003119134-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1269

ID ADH38190 standard; protein; 1092 AA.

DE Novel human secreted and transmembrane protein PRO34001.

PN US2003119123-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1270

ID ADH38886 standard; protein; 1092 AA.

DE Human secreted/transmembrane polypeptide PRO34001.

PN US2003119141-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1271

ID ADH23824 standard; protein; 1092 AA.

DE Human secreted/transmembrane polypeptide PRO34001.

PN US2003119142-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1272

ID ADH40199 standard; protein; 1092 AA.

DE Human PRO34001 protein.

PN US2003119132-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1273

ID ADH40084 standard; protein; 1092 AA.
 DE Human PRO34001 protein.
 PN US2003119133-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1274

ID ADH31406 standard; protein; 1092 AA.
 DE Human PRO polypeptide #48.
 PN US2003119138-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1275

ID ADH29284 standard; protein; 1092 AA.
 DE Human secreted/transmembrane polypeptide PRO34001.
 PN US2003119136-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1276

ID ADH49499 standard; protein; 1092 AA.
 DE Novel human secreted and transmembrane protein PRO34001.
 PN US2003119127-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1277

ID ADH51963 standard; protein; 1092 AA.
 DE Novel human secreted and transmembrane protein PRO34001.
 PN US2003119125-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1278

ID ADH49818 standard; protein; 1092 AA.
 DE Novel human secreted and transmembrane protein PRO34001.
 PN US2003119128-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;
 Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1279

ID ADH52419 standard; protein; 1092 AA.
 DE Novel human secreted and transmembrane protein PRO34001.
 PN US2003119130-A1.
 PD 26-JUN-2003.
 PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1280

ID ADH52535 standard; protein; 1092 AA.

DE Novel human secreted and transmembrane protein PRO34001.

PN US2003119129-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1281

ID ADH58532 standard; protein; 1092 AA.

DE Novel human secreted and transmembrane protein PRO34001.

PN US2003119121-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1282

ID ADH51847 standard; protein; 1092 AA.

DE Novel human secreted and transmembrane protein PRO34001.

PN US2003119126-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1283

ID ADH58408 standard; protein; 1092 AA.

DE Novel human secreted and transmembrane protein PRO34001.

PN US2003119122-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1284

ID ADI13605 standard; protein; 1092 AA.

DE Novel human secreted and transmembrane protein PRO34001.

PN US2003119131-A1.

PD 26-JUN-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1285

ID ADK00861 standard; protein; 1092 AA.

DE Human PRO polypeptide #48.

PN US2003186373-A1.

PD 02-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1286

ID ADL08602 standard; protein; 1092 AA.

DE Human secreted/transmembrane polypeptide PRO34001.

PN US2003186372-A1.

PD 02-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;

Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1287

ID ADL06554 standard; protein; 1092 AA.
DE Human tumour-associated antigenic target (TAT) polypeptide #53.
PN WO2004016225-A2.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.

Query Match 17.9%; Score 721.5; DB 8; Length 1092;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1288

ID AAG68290 standard; protein; 1093 AA.
DE Human semaphorin G-like NHP protein SEQ ID NO:4.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.

Query Match 17.9%; Score 721.5; DB 5; Length 1093;
Best Local Similarity 34.6%; Pred. No. 2.5e-63;

RESULT 1289

ID AAG68294 standard; protein; 1136 AA.
DE Human semaphorin G-like NHP protein SEQ ID NO:12.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.

Query Match 17.9%; Score 721.5; DB 5; Length 1136;
Best Local Similarity 34.6%; Pred. No. 2.6e-63;

RESULT 1290

ID AAG68293 standard; protein; 1151 AA.
DE Human semaphorin G-like NHP protein SEQ ID NO:10.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.

Query Match 17.9%; Score 721.5; DB 5; Length 1151;
Best Local Similarity 34.6%; Pred. No. 2.7e-63;

RESULT 1291

ID AAG68298 standard; protein; 496 AA.
DE Human semaphorin G-like NHP protein SEQ ID NO:21.
PN WO200188133-A2.
PD 22-NOV-2001.
PA (LEXI-) LEXICON GENETICS INC.

Query Match 17.6%; Score 710; DB 5; Length 496;
Best Local Similarity 38.6%; Pred. No. 9.9e-63;

RESULT 1292

ID AAW63748 standard; protein; 775 AA.
DE Human semaphorin.
PN WO9822504-A1.
PD 28-MAY-1998.
PA (SUMU) SUMITOMO PHARM CO LTD.

Query Match 17.6%; Score 709.5; DB 2; Length 775;
Best Local Similarity 29.4%; Pred. No. 2.4e-62;

RESULT 1293

ID AAY43090 standard; protein; 775 AA.
DE Mouse semaphorin H (Sema H) amino acid sequence.
PN WO9947671-A2.
PD 23-SEP-1999.
PA (LUKA/) LUKANIDIN E M.
PA (CHRI/) CHRISTENSEN C R L.

Query Match 17.4%; Score 702.5; DB 2; Length 775;
Best Local Similarity 28.7%; Pred. No. 1.2e-61;

RESULT 1294

ID ADI79363 standard; protein; 775 AA.
DE Mouse Sema3E amino acid sequence SEQ ID NO:1.
PN WO2004006898-A2.
PD 22-JAN-2004.
PA (SEMA-) SEMA APS.

Query Match 17.4%; Score 702.5; DB 8; Length 775;
Best Local Similarity 28.7%; Pred. No. 1.2e-61;

RESULT 1295

ID AAB84219 standard; protein; 779 AA.
DE Amino acid sequence of a semaphorin polypeptide designated ZSMF-16.
PN WO200140278-A2.
PD 07-JUN-2001.
PA (ZYMO) ZYMOGENETICS INC.

Query Match 17.4%; Score 702.5; DB 4; Length 779;
Best Local Similarity 27.8%; Pred. No. 1.2e-61;

RESULT 1296

ID AAG78481 standard; protein; 779 AA.
DE Human ZSMF-16.
PN US2001049432-A1.
PD 06-DEC-2001.
PA (HOLL/) HOLLOWAY J L.
PA (FOLE/) FOLEY K P.

Query Match 17.4%; Score 702.5; DB 5; Length 779;
Best Local Similarity 27.8%; Pred. No. 1.2e-61;

RESULT 1297

ID ABR47588 standard; protein; 775 AA.
DE Breast cancer associated protein sequence SEQ ID NO:415.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.

Query Match 17.4%; Score 700.5; DB 6; Length 775;
Best Local Similarity 29.0%; Pred. No. 2e-61;

RESULT 1298

ID ADD08940 standard; protein; 775 AA.
DE Human semaphorin 3E protein SEQ ID NO:16.
PN WO2003029814-A2.
PD 10-APR-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.

Query Match 17.4%; Score 700.5; DB 7; Length 775;
Best Local Similarity 29.0%; Pred. No. 2e-61;

RESULT 1299

ID ADG76179 standard; protein; 775 AA.
DE Human NOVX protein to treat human pathological conditions (SeqID 92).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.

Query Match 17.4%; Score 700.5; DB 7; Length 775;
Best Local Similarity 29.0%; Pred. No. 2e-61;

RESULT 1300

ID ADG76185 standard; protein; 775 AA.
DE Human NOVX protein to treat human pathological conditions (SeqID 98).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.

Query Match 17.4%; Score 700.5; DB 7; Length 775;

Best Local Similarity 29.0%; Pred. No. 2e-61;
 RESULT 1301
 ID ADG76181 standard; protein; 775 AA.
 DE Human NOVX protein to treat human pathological conditions (SeqID 94).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 17.4%; Score 700.5; DB 7; Length 775;
 Best Local Similarity 29.0%; Pred. No. 2e-61;
 RESULT 1302
 ID ADG76183 standard; protein; 775 AA.
 DE Human NOVX protein to treat human pathological conditions (SeqID 96).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 17.4%; Score 700.5; DB 7; Length 775;
 Best Local Similarity 29.0%; Pred. No. 2e-61;
 RESULT 1303
 ID ADI79364 standard; protein; 775 AA.
 DE Human Sema3E amino acid sequence SEQ ID NO:2.
 PN WO2004006898-A2.
 PD 22-JAN-2004.
 PA (SEMA-) SEMA APS.
 Query Match 17.4%; Score 700.5; DB 8; Length 775;
 Best Local Similarity 29.0%; Pred. No. 2e-61;
 RESULT 1304
 ID AAW51314 standard; protein; 587 AA.
 DE Human semaphorin W.
 PN WO9815628-A1.
 PD 16-APR-1998.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Query Match 17.2%; Score 695; DB 2; Length 587;
 Best Local Similarity 33.1%; Pred. No. 4.5e-61;
 RESULT 1305
 ID AAE02455 standard; protein; 1093 AA.
 DE Mouse semaphorin G protein.
 PN WO200132707-A1.
 PD 10-MAY-2001.
 PA (ZYMO) ZYMOGENETICS INC.
 Query Match 17.2%; Score 694; DB 4; Length 1093;
 Best Local Similarity 35.1%; Pred. No. 1.6e-60;
 RESULT 1306
 ID ADG76141 standard; protein; 878 AA.
 DE Human NOVX protein to treat human pathological conditions (SeqID 54).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 17.1%; Score 690.5; DB 7; Length 878;
 Best Local Similarity 28.4%; Pred. No. 2.6e-60;
 RESULT 1307
 ID ADF45364 standard; protein; 878 AA.
 DE Human semaphorin-like protein NOV2u protein SEQ ID NO:54.
 PN WO2003102584-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 17.1%; Score 690.5; DB 8; Length 878;
 Best Local Similarity 28.4%; Pred. No. 2.6e-60;

RESULT 1308

ID ADO40298 standard; protein; 878 AA.
 DE Human semaphorin-like protein NOV2u.
 PN US2004018977-A1.
 PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.

Query Match 17.1%; Score 690.5; DB 8; Length 878;
 Best Local Similarity 28.4%; Pred. No. 2.6e-60;

RESULT 1309

ID ADG76139 standard; protein; 861 AA.
 DE Human NOVX protein to treat human pathological conditions (SeqID 52).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.

Query Match 17.0%; Score 687; DB 7; Length 861;
 Best Local Similarity 30.5%; Pred. No. 5.6e-60;

RESULT 1310

ID ADF45362 standard; protein; 861 AA.
 DE Human semaphorin-like protein NOV2t protein SEQ ID NO:52.
 PN WO2003102584-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.

Query Match 17.0%; Score 687; DB 8; Length 861;
 Best Local Similarity 30.5%; Pred. No. 5.6e-60;

RESULT 1311

ID ADO40296 standard; protein; 861 AA.
 DE Human semaphorin-like protein NOV2t.
 PN US2004018977-A1.
 PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.

Query Match 17.0%; Score 687; DB 8; Length 861;
 Best Local Similarity 30.5%; Pred. No. 5.6e-60;

RESULT 1312

ID AAY43091 standard; protein; 777 AA.
 DE Mouse semaphorin H variant (Sema Hv) amino acid sequence.
 PN WO9947671-A2.
 PD 23-SEP-1999.

PA (LUKA/) LUKANIDIN E M.
PA (CHRI/) CHRISTENSEN C R L.
Query Match 16.9%; Score 682; DB 2; Length 777;
Best Local Similarity 29.1%; Pred. No. 1.5e-59;
RESULT 1313
ID AAG62730 standard; peptide; 777 AA.
DE Amino acid sequence of mouse semaphorin Sema3E.
PN WO200138491-A2.
PD 31-MAY-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 16.9%; Score 682; DB 4; Length 777;
Best Local Similarity 29.1%; Pred. No. 1.5e-59;
RESULT 1314
ID ADG76107 standard; protein; 998 AA.
DE Human NOVX protein to treat human pathological conditions (SeqID 20).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.9%; Score 680; DB 7; Length 998;
Best Local Similarity 28.5%; Pred. No. 3.8e-59;
RESULT 1315
ID ADF45330 standard; protein; 998 AA.
DE Human semaphorin-like protein NOV2d protein SEQ ID NO:20.
PN WO2003102584-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.9%; Score 680; DB 8; Length 998;
Best Local Similarity 28.5%; Pred. No. 3.8e-59;
RESULT 1316
ID ADO40264 standard; protein; 998 AA.
DE Human semaphorin-like protein NOV2d.
PN US2004018977-A1.
PD 29-JAN-2004.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.
Query Match 16.9%; Score 680; DB 8; Length 998;
Best Local Similarity 28.5%; Pred. No. 3.8e-59;
RESULT 1317
ID ADG76105 standard; protein; 1035 AA.
DE Human NOVX protein to treat human pathological conditions (SeqID 18).
PN WO2003085096-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.9%; Score 680; DB 7; Length 1035;
Best Local Similarity 28.5%; Pred. No. 4e-59;
RESULT 1318
ID ADF45328 standard; protein; 1035 AA.
DE Human semaphorin-like protein NOV2c protein SEQ ID NO:18.

PN WO2003102584-A2.

PD 11-DEC-2003.

PA (CURA-) CURAGEN CORP.

Query Match 16.9%; Score 680; DB 8; Length 1035;

Best Local Similarity 28.5%; Pred. No. 4e-59;

RESULT 1319

ID ADO40262 standard; protein; 1035 AA.

DE Human semaphorin-like protein NOV2c.

PN US2004018977-A1.

PD 29-JAN-2004.

PA (ALVA/) ALVAREZ E.

PA (ANDE/) ANDERSON D W.

PA (DHAN/) DHANABAL M.

PA (KHRA/) KHRAMTSOV N V.

PA (LARO/) LAROCHELLE W J.

PA (LICH/) LICHENSTEIN H S.

PA (LILL/) LI L.

PA (OOIC/) OOI C E.

PA (PADI/) PADIGARU M.

PA (SHIM/) SHIMKETS R A.

PA (ZHON/) ZHONG M.

Query Match 16.9%; Score 680; DB 8; Length 1035;

Best Local Similarity 28.5%; Pred. No. 4e-59;

RESULT 1320

ID ADG76101 standard; protein; 1047 AA.

DE Human NOVX protein to treat human pathological conditions (SeqID 14).

PN WO2003085096-A2.

PD 16-OCT-2003.

PA (CURA-) CURAGEN CORP.

Query Match 16.9%; Score 680; DB 7; Length 1047;

Best Local Similarity 28.5%; Pred. No. 4.1e-59;

RESULT 1321

ID ADG76135 standard; protein; 1047 AA.

DE Human NOVX protein to treat human pathological conditions (SeqID 48).

PN WO2003085096-A2.

PD 16-OCT-2003.

PA (CURA-) CURAGEN CORP.

Query Match 16.9%; Score 680; DB 7; Length 1047;

Best Local Similarity 28.5%; Pred. No. 4.1e-59;

RESULT 1322

ID ADF45324 standard; protein; 1047 AA.

DE Human semaphorin-like protein NOV2a protein SEQ ID NO:14.

PN WO2003102584-A2.

PD 11-DEC-2003.

PA (CURA-) CURAGEN CORP.

Query Match 16.9%; Score 680; DB 8; Length 1047;

Best Local Similarity 28.5%; Pred. No. 4.1e-59;

RESULT 1323

ID ADF45358 standard; protein; 1047 AA.

DE Human semaphorin-like protein NOV2r protein SEQ ID NO:48.

PN WO2003102584-A2.

PD 11-DEC-2003.

PA (CURA-) CURAGEN CORP.

Query Match 16.9%; Score 680; DB 8; Length 1047;

Best Local Similarity 28.5%; Pred. No. 4.1e-59;

RESULT 1324

ID ADM35787 standard; protein; 1047 AA.

DE Novel human NOVX protein for treating diabetes and obesity.
PN WO2004013347-A2.
PD 12-FEB-2004.
PA (CURA-) CURAGEN CORP.

Query Match 16.9%; Score 680; DB 8; Length 1047;
Best Local Similarity 28.5%; Pred. No. 4.1e-59;

RESULT 1325

ID ADO40258 standard; protein; 1047 AA.
DE Human semaphorin-like protein NOV2a.
PN US2004018977-A1.
PD 29-JAN-2004.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.

Query Match 16.9%; Score 680; DB 8; Length 1047;
Best Local Similarity 28.5%; Pred. No. 4.1e-59;

RESULT 1326

ID ADO40292 standard; protein; 1047 AA.
DE Human semaphorin-like protein NOV2r.
PN US2004018977-A1.
PD 29-JAN-2004.
PA (ALVA/) ALVAREZ E.
PA (ANDE/) ANDERSON D W.
PA (DHAN/) DHANABAL M.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LICH/) LICHENSTEIN H S.
PA (LILL/) LI L.
PA (OOIC/) OOI C E.
PA (PADI/) PADIGARU M.
PA (SHIM/) SHIMKETS R A.
PA (ZHON/) ZHONG M.

Query Match 16.9%; Score 680; DB 8; Length 1047;
Best Local Similarity 28.5%; Pred. No. 4.1e-59;

RESULT 1327

ID ADQ19981 standard; protein; 1049 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2801.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 16.9%; Score 680; DB 8; Length 1049;
Best Local Similarity 28.5%; Pred. No. 4.1e-59;

RESULT 1328

ID ABO84445 standard; protein; 879 AA.
DE Mouse cancer-associated protein MP7-239.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 16.8%; Score 678.5; DB 8; Length 879;

Best Local Similarity 32.8%; Pred. No. 4.3e-59;
 RESULT 1329
 ID ADG76143 standard; protein; 666 AA.
 DE Human NOVX protein to treat human pathological conditions (SeqID 56).
 PN WO2003085096-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 16.8%; Score 678; DB 7; Length 666;
 Best Local Similarity 28.6%; Pred. No. 3e-59;
 RESULT 1330
 ID ADF45366 standard; protein; 666 AA.
 DE Human semaphorin-like protein NOV2v protein SEQ ID NO:56.
 PN WO2003102584-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 16.8%; Score 678; DB 8; Length 666;
 Best Local Similarity 28.6%; Pred. No. 3e-59;
 RESULT 1331
 ID ADO40300 standard; protein; 666 AA.
 DE Human semaphorin-like protein NOV2v.
 PN US2004018977-A1.
 PD 29-JAN-2004.
 PA (ALVA/) ALVAREZ E.
 PA (ANDE/) ANDERSON D W.
 PA (DHAN/) DHANABAL M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LICH/) LICHENSTEIN H S.
 PA (LILL/) LI L.
 PA (OOIC/) OOI C E.
 PA (PADI/) PADIGARU M.
 PA (SHIM/) SHIMKETS R A.
 PA (ZHON/) ZHONG M.
 Query Match 16.8%; Score 678; DB 8; Length 666;
 Best Local Similarity 28.6%; Pred. No. 3e-59;
 RESULT 1332
 ID ADI79365 standard; protein; 560 AA.
 DE 61 kDa proteolytic fragment of mouse Sema3E SEQ ID NO:3.
 PN WO2004006898-A2.
 PD 22-JAN-2004.
 PA (SEMA-) SEMA APS.
 Query Match 16.8%; Score 677.5; DB 8; Length 560;
 Best Local Similarity 31.7%; Pred. No. 2.6e-59;
 RESULT 1333
 ID ADD14122 standard; protein; 1074 AA.
 DE Human src biomarker polypeptide SEQ ID NO:311.
 PN WO2003062395-A2.
 PD 31-JUL-2003.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 16.8%; Score 677.5; DB 7; Length 1074;
 Best Local Similarity 34.1%; Pred. No. 7.7e-59;
 RESULT 1334
 ID ADQ21454 standard; protein; 1074 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4274.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 16.8%; Score 677.5; DB 8; Length 1074;
Best Local Similarity 34.1%; Pred. No. 7.7e-59;
RESULT 1335

ID AAU32291 standard; protein; 1075 AA.
DE Novel human secreted protein #2782.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 16.8%; Score 677.5; DB 4; Length 1075;
Best Local Similarity 34.1%; Pred. No. 7.7e-59;

RESULT 1336

ID ADI79366 standard; protein; 560 AA.
DE 61 kDa proteolytic fragment of human Sema3E SEQ ID NO:4.
PN WO2004006898-A2.
PD 22-JAN-2004.
PA (SEMA-) SEMA APS.

Query Match 16.8%; Score 677; DB 8; Length 560;
Best Local Similarity 31.2%; Pred. No. 2.9e-59;

RESULT 1337

ID AAB18916 standard; protein; 888 AA.
DE A novel polypeptide designated PRO4353.
PN WO200056889-A2.
PD 28-SEP-2000.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 3; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1338

ID AAU12443 standard; protein; 888 AA.
DE Human PRO4353 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 4; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1339

ID ABB84950 standard; protein; 888 AA.
DE Human PRO4353 protein sequence SEQ ID NO:268.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 5; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1340

ID ABB95556 standard; protein; 888 AA.
DE Human angiogenesis related protein PRO4353 SEQ ID NO: 268.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 16.8%; Score 676; DB 5; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1341
 ID ABO17887 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1342
 ID ABU69110 standard; protein; 888 AA.
 DE Human PRO polypeptide #8.
 PN US2003032061-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1343
 ID ABU81141 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003004311-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1344
 ID ABO19426 standard; protein; 888 AA.
 DE Human secreted / transmembrane polypeptide PRO1353.
 PN US2003027249-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1345
 ID ABU66841 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1346
 ID ABU59922 standard; protein; 888 AA.
 DE Novel secreted and transmembrane protein PRO4353.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1347

ID ABU69087 standard; protein; 888 AA.
 DE Human PRO polypeptide #8.
 PN US2003008348-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1348
 ID ABO25112 standard; protein; 888 AA.
 DE Human secreted/transmembrane protein (PRO) #272.
 PN US2003036179-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1349
 ID ABU67117 standard; protein; 888 AA.
 DE Human secreted/transmembrane, PRO, protein SEQ ID 544.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1350
 ID ABU81551 standard; protein; 888 AA.
 DE Human secreted polypeptide PRO4353.
 PN US2002192751-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1351
 ID ADA46063 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003022328-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1352
 ID ADA76560 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003036114-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1353
 ID ADA76494 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003073212-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1354
 ID ADA19144 standard; protein; 888 AA.

DE Human PRO polypeptide #272.
 PN US2003054517-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1355
 ID ADA61767 standard; protein; 888 AA.
 DE Homo sapiens.
 PN US2003049816-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1356
 ID ADB19552 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003068796-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1357
 ID ADB28093 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003082704-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1358
 ID ADA86572 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003082711-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1359
 ID ADB16136 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003087350-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1360
 ID ADA47922 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003073215-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1361
 ID ADA67717 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.

PN US2003068795-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1362
 ID ADB30724 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003068794-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1363
 ID ADA86020 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003082693-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1364
 ID ADA97232 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003082705-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1365
 ID ADA79536 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003082763-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1366
 ID ADA87675 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003087345-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1367
 ID ADB16877 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003087349-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1368
 ID ADA91969 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003082694-A1.

PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1369
 ID ADB15032 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003087351-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1370
 ID ADB18993 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003073211-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1371
 ID ADA94208 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003077722-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1372
 ID ADB20104 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003082691-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1373
 ID ADB13416 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003082710-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1374
 ID ABO43420 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003044945-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1375
 ID ADA74670 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003068798-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1376

ID ADB24903 standard; protein; 888 AA.

DE Human PRO polypeptide SEQ ID NO 544.

PN US2003077713-A1.

PD 24-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1377

ID ADA82427 standard; protein; 888 AA.

DE Human PRO polypeptide #272.

PN US2003082701-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1378

ID ADA75390 standard; protein; 888 AA.

DE Human PRO polypeptide #272.

PN US2003073216-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1379

ID ADA85468 standard; protein; 888 AA.

DE Novel human secreted and transmembrane protein PRO4353.

PN US2003082695-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1380

ID ADA84916 standard; protein; 888 AA.

DE Novel human secreted and transmembrane protein PRO4353.

PN US2003082708-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1381

ID ADB30172 standard; protein; 888 AA.

DE Human PRO polypeptide #272.

PN US2003073214-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1382

ID ADA80700 standard; protein; 888 AA.

DE Human PRO polypeptide #272.

PN US2003082761-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1383
 ID ADA75942 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003082703-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1384
 ID ADA47167 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003073210-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1385
 ID ADB25463 standard; protein; 888 AA.
 DE Human PRO polypeptide SEQ ID NO 544.
 PN US2003077715-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1386
 ID ADA93639 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003077721-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1387
 ID ADB26989 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003092147-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1388
 ID ADB31276 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003096386-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1389
 ID ADA61204 standard; protein; 888 AA.
 DE Homo sapiens.
 PN US2003049817-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 6; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1390
ID ADB24351 standard; protein; 888 AA.
DE Human PRO polypeptide SEQ ID NO 544.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1391
ID ADA96680 standard; protein; 888 AA.
DE Human PRO polypeptide #272.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1392
ID ADA81252 standard; protein; 888 AA.
DE Human PRO polypeptide #272.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1393
ID ADA96128 standard; protein; 888 AA.
DE Human PRO polypeptide #272.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1394
ID ADB26437 standard; protein; 888 AA.
DE Human PRO polypeptide #272.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1395
ID ADB21922 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein PRO4353.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 6; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1396
ID ADA77701 standard; protein; 888 AA.
DE Human PRO polypeptide #272.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1397

ID ADB18441 standard; protein; 888 AA.

DE Human PRO polypeptide #272.

PN US2003077710-A1.

PD 24-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1398

ID ADA87124 standard; protein; 888 AA.

DE Novel human secreted and transmembrane protein PRO4353.

PN US2003082709-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1399

ID ABO25134 standard; protein; 888 AA.

DE Human secreted/transmembrane protein PRO4353.

PN US2003044842-A1.

PD 06-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1400

ID ADA88227 standard; protein; 888 AA.

DE Novel human secreted and transmembrane protein PRO4353.

PN US2003082700-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1401

ID ADA46615 standard; protein; 888 AA.

DE Novel human secreted and transmembrane protein PRO4353.

PN US2003054516-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1402

ID ADB28645 standard; protein; 888 AA.

DE Human PRO polypeptide #272.

PN US2003082699-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1403

ID ADB29197 standard; protein; 888 AA.

DE Human PRO polypeptide #272.

PN US2003082706-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1404

ID ADA77149 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003059909-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1405
 ID ADA88779 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003073213-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1406
 ID ADA97784 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003082686-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1407
 ID ADB27541 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003022239-A1.
 PD 30-JAN-2003.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1408
 ID ADB22474 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003087344-A1.
 PD 08-MAY-2003.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1409
 ID ADA67165 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003068793-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1410
 ID ADB23026 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003077711-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1411
 ID ADB23799 standard; protein; 888 AA.
 DE Human PRO polypeptide SEQ ID NO 544.
 PN US2003077712-A1.

PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1412
 ID ADA92521 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003082712-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1413
 ID ADB15584 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003087352-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1414
 ID ADB38836 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003082766-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1415
 ID ADB38284 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003087347-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1416
 ID ADB66756 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003082689-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1417
 ID ADB89836 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003082698-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1418
 ID ADB90568 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003082762-A1.
 PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1419
 ID ADB39669 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003082764-A1.
 PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1420
 ID ADB47292 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003082687-A1.
 PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1421
 ID ADB86899 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003082697-A1.
 PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1422
 ID ADB77504 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003082696-A1.
 PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1423
 ID ADB34661 standard; protein; 888 AA.
 DE Human PRO polypeptide SEQ ID NO 544.
 PN US2003077717-A1.
 PD 24-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1424
 ID ADB35765 standard; protein; 888 AA.
 DE Human PRO polypeptide SEQ ID NO 544.
 PN US2003077719-A1.
 PD 24-APR-2003.

PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1425
 ID ADB34109 standard; protein; 888 AA.
 DE Human PRO polypeptide SEQ ID NO 544.
 PN US2003077716-A1.
 PD 24-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1426

ID ADB35213 standard; protein; 888 AA.
DE Human PRO polypeptide SEQ ID NO 544.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1427

ID ADB36317 standard; protein; 888 AA.
DE Human PRO polypeptide SEQ ID NO 544.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1428

ID ADB46712 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein PRO4353.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1429

ID AAE39104 standard; protein; 888 AA.
DE Human PRO4353 protein.
PN US2003049733-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1430

ID AAE39041 standard; protein; 888 AA.
DE Human PRO4353 protein.
PN US2003049734-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1431

ID ADC50585 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein PRO4353.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;
RESULT 1432

ID ADC72132 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein PRO4353.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1433
 ID ADC29791 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003092063-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1434
 ID ADC60111 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003092105-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1435
 ID ADC53118 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein Seq ID544.
 PN US2003087365-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1436
 ID ADC57472 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein Seq ID544.
 PN US2003087366-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1437
 ID ADC60663 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003087367-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1438
 ID ADC51138 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003087361-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1439
 ID ADC65665 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003087362-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1440

ID ADC54763 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein Seq ID544.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1441

ID ADC53724 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein Seq ID544.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1442

ID ADC59247 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein Seq ID544.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1443

ID ADC56125 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein Seq ID544.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1444

ID ADC58695 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein Seq ID544.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1445

ID ADD03369 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein PRO4353.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1446

ID ADC90361 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein PRO4353.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1447

ID ADC69780 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003194770-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1448
 ID ADC48669 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003194773-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1449
 ID ADD10198 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003194776-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1450
 ID ADD04773 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003087354-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1451
 ID ADC80729 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003092103-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1452
 ID ADD11236 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003194774-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1453
 ID ADD10557 standard; protein; 888 AA.
 DE Human secreted/transmembrane PRO polypeptide #134.
 PN US2003105011-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1454
 ID ADC48117 standard; protein; 888 AA.

DE Human PRO polypeptide #272.
 PN US2003194771-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1455
 ID ADC80177 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003087358-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1456
 ID ADD11517 standard; protein; 888 AA.
 DE Human secreted/transmembrane PRO polypeptide #134.
 PN US2003105013-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1457
 ID ADD09646 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003194775-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1458
 ID ADD41359 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003203438-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1459
 ID ADD52498 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003194769-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1460
 ID ADD53238 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003194792-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1461
 ID ADD53790 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.

PN US2003203437-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1462
 ID ADD37310 standard; protein; 888 AA.
 DE Human secreted/transmembrane PRO polypeptide #134.
 PN US2003105012-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1463
 ID ADD51946 standard; protein; 888 AA.
 DE Human PRO polypeptide #272..
 PN US2003194779-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1464
 ID ADD02745 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003203431-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1465
 ID ADD02179 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003203430-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1466
 ID ADD54361 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003203432-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1467
 ID ADD92678 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003199030-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1468
 ID ADD91574 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003199055-A1.

PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1469
 ID ADE04188 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003199057-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1470
 ID ADE32485 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003194765-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1471
 ID ADE22417 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003199056-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1472
 ID ADD79641 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003203428-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1473
 ID ADE42177 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003194772-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1474
 ID ADE17994 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003199023-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1475
 ID ADD92126 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003199053-A1.
 PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1476
 ID ADE33589 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003194767-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1477
 ID ADE34141 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003194791-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1478
 ID ADD80193 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003207417-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1479
 ID ADD93230 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003194768-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1480
 ID ADE19650 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003199025-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1481
 ID ADE19098 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003199026-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1482
 ID ADE43294 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003199033-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1483

ID ADD96083 standard; protein; 888 AA.
DE Human PRO polypeptide #272.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1484

ID ADE22969 standard; protein; 888 AA.
DE Human PRO polypeptide #272.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1485

ID ADD79087 standard; protein; 888 AA.
DE Human PRO polypeptide #272.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1486

ID ADE33037 standard; protein; 888 AA.
DE Novel human secreted and transmembrane protein PRO4353.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1487

ID ADE42729 standard; protein; 888 AA.
DE Human PRO polypeptide #272.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1488

ID ADD80745 standard; protein; 888 AA.
DE Human PRO polypeptide #272.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;
Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1489

ID ADD89773 standard; protein; 888 AA.
DE Human PRO polypeptide #272.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1490
 ID ADE41057 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003199031-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1491
 ID ADE04856 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003199034-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1492
 ID ADE92985 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003194777-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1493
 ID ADG21694 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003207355-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1494
 ID ADG23335 standard; protein; 888 AA.
 DE Novel human secreted and transmembrane protein PRO4353.
 PN US2003207384-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1495
 ID ADF97670 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003207370-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;
 RESULT 1496
 ID ADG80734 standard; protein; 888 AA.
 DE Human PRO polypeptide #272.
 PN US2003207373-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 16.8%; Score 676; DB 7; Length 888;
 Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1497

ID ADG80182 standard; protein; 888 AA.

DE Human PRO polypeptide #272.

PN US2003207372-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1498

ID ADH55474 standard; protein; 888 AA.

DE Novel human secreted and transmembrane protein PRO4353.

PN US2003207381-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1499

ID ADH56026 standard; protein; 888 AA.

DE Novel human secreted and transmembrane protein PRO4353.

PN US2003207379-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;

RESULT 1500

ID ADI64245 standard; protein; 888 AA.

DE Novel human secreted and transmembrane protein PRO4353.

PN US2003207385-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 16.8%; Score 676; DB 7; Length 888;

Best Local Similarity 27.1%; Pred. No. 7.9e-59;

OM protein - protein search, using sw model

Run on: February 10, 2005, 02:08:58 ; Search time 44 Seconds
(without alignments)
1291.089 Million cell updates/sec

Title: US-10-015-391A-277
Perfect score: 4031
Sequence: 1 MALPALGLDPWSLLGLFLFQ.....CRTSASDVDADNNCLGTEVA 761

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	4031	100.0	761	4	US-09-578-063-19	Sequence 19, Appl
2	3875	96.1	730	4	US-09-578-063-21	Sequence 21, Appl
3	3486	86.5	652	4	US-09-578-063-22	Sequence 22, Appl
4	3280.5	81.4	760	4	US-09-578-063-70	Sequence 70, Appl
5	3280.5	81.4	760	4	US-09-578-063-76	Sequence 76, Appl
6	1150.5	28.5	607	4	US-08-556-422A-4	Sequence 4, Appli
7	1044	25.9	862	4	US-08-556-422A-2	Sequence 2, Appli
8	961	23.8	865	4	US-09-854-845-33	Sequence 33, Appl
9	958	23.8	838	4	US-09-854-845-29	Sequence 29, Appl
10	954.5	23.7	870	4	US-09-854-845-31	Sequence 31, Appl
11	951.5	23.6	843	4	US-09-854-845-27	Sequence 27, Appl

12	895	22.2	766	4	US-09-854-845-49	Sequence 49, Appl
13	893	22.2	697	4	US-09-854-845-25	Sequence 25, Appl
14	892	22.1	739	4	US-09-854-845-45	Sequence 45, Appl
15	888.5	22.0	771	4	US-09-854-845-47	Sequence 47, Appl
16	886.5	22.0	702	4	US-09-854-845-23	Sequence 23, Appl
17	885.5	22.0	744	4	US-09-854-845-43	Sequence 43, Appl
18	827	20.5	598	4	US-09-854-845-41	Sequence 41, Appl
19	825.5	20.5	771	1	US-08-121-713D-54	Sequence 54, Appl
20	825.5	20.5	771	1	US-08-835-268-54	Sequence 54, Appl
21	825.5	20.5	771	2	US-09-060-692-54	Sequence 54, Appl
22	825.5	20.5	771	3	US-08-833-391-54	Sequence 54, Appl
23	825.5	20.5	771	3	US-09-060-610-54	Sequence 54, Appl
24	825.5	20.5	771	5	PCT-US94-10151A-54	Sequence 54, Appl
25	820.5	20.4	603	4	US-09-854-845-39	Sequence 39, Appl
26	815.5	20.2	655	4	US-08-556-422A-3	Sequence 3, Appli
27	737	18.3	782	4	US-09-813-290-4	Sequence 4, Appli
28	737	18.3	875	4	US-09-813-290-2	Sequence 2, Appli
29	721.5	17.9	1034	4	US-09-854-845-6	Sequence 6, Appli
30	721.5	17.9	1049	4	US-09-854-845-2	Sequence 2, Appli
31	721.5	17.9	1078	4	US-09-854-845-8	Sequence 8, Appli
32	721.5	17.9	1093	4	US-09-854-845-4	Sequence 4, Appli
33	721.5	17.9	1136	4	US-09-854-845-12	Sequence 12, Appl
34	721.5	17.9	1151	4	US-09-854-845-10	Sequence 10, Appl
35	710	17.6	496	4	US-09-854-845-21	Sequence 21, Appl
36	709.5	17.6	775	4	US-09-308-179B-1	Sequence 1, Appli
37	699	17.3	425	4	US-08-556-422A-7	Sequence 7, Appli
38	673	16.7	888	4	US-09-077-940A-4	Sequence 4, Appli
39	672.5	16.7	887	4	US-09-077-940A-2	Sequence 2, Appli
40	671	16.6	630	4	US-09-520-781-30	Sequence 30, Appl
41	671	16.6	884	4	US-09-520-781-6	Sequence 6, Appli
42	671	16.6	939	4	US-09-520-781-4	Sequence 4, Appli
43	666	16.5	1070	4	US-09-653-274-8	Sequence 8, Appli
44	666	16.5	1070	4	US-10-461-791-8	Sequence 8, Appli
45	666	16.5	1086	4	US-09-653-274-4	Sequence 4, Appli
46	666	16.5	1086	4	US-10-461-791-4	Sequence 4, Appli
47	655	16.2	641	4	US-09-653-274-13	Sequence 13, Appl
48	655	16.2	641	4	US-10-461-791-13	Sequence 13, Appl
49	653.5	16.2	730	1	US-08-121-713D-58	Sequence 58, Appl
50	653.5	16.2	730	1	US-08-835-268-58	Sequence 58, Appl
51	653.5	16.2	730	2	US-09-060-692-58	Sequence 58, Appl
52	653.5	16.2	730	3	US-08-833-391-58	Sequence 58, Appl
53	653.5	16.2	730	3	US-09-060-610-58	Sequence 58, Appl
54	653.5	16.2	730	5	PCT-US94-10151A-58	Sequence 58, Appl
55	644	16.0	397	4	US-09-854-845-37	Sequence 37, Appl
56	629	15.6	930	4	US-09-254-594-6	Sequence 6, Appli
57	625	15.5	939	4	US-09-854-845-16	Sequence 16, Appl
58	625	15.5	954	4	US-09-854-845-14	Sequence 14, Appl
59	615.5	15.3	536	4	US-09-653-274-10	Sequence 10, Appl
60	615.5	15.3	536	4	US-10-461-791-10	Sequence 10, Appl
61	604	15.0	712	1	US-08-121-713D-64	Sequence 64, Appl
62	604	15.0	712	1	US-08-835-268-64	Sequence 64, Appl
63	604	15.0	712	2	US-09-060-692-64	Sequence 64, Appl
64	604	15.0	712	3	US-08-833-391-64	Sequence 64, Appl
65	604	15.0	712	3	US-09-060-610-64	Sequence 64, Appl
66	604	15.0	712	5	PCT-US94-10151A-64	Sequence 64, Appl
67	600.5	14.9	724	1	US-08-121-713D-62	Sequence 62, Appl
68	600.5	14.9	724	1	US-08-835-268-62	Sequence 62, Appl

69	600.5	14.9	724	2	US-09-060-692-62	Sequence 62, Appl
70	600.5	14.9	724	3	US-08-833-391-62	Sequence 62, Appl
71	600.5	14.9	724	3	US-09-060-610-62	Sequence 62, Appl
72	600.5	14.9	724	5	PCT-US94-10151A-62	Sequence 62, Appl
73	600	14.9	650	1	US-08-121-713D-60	Sequence 60, Appl
74	600	14.9	650	1	US-08-835-268-60	Sequence 60, Appl
75	600	14.9	650	2	US-09-060-692-60	Sequence 60, Appl
76	600	14.9	650	3	US-08-833-391-60	Sequence 60, Appl
77	600	14.9	650	3	US-09-060-610-60	Sequence 60, Appl
78	600	14.9	650	5	PCT-US94-10151A-60	Sequence 60, Appl
79	587	14.6	295	4	US-08-556-422A-6	Sequence 6, Appli
80	584	14.5	929	4	US-09-254-594-3	Sequence 3, Appli
81	526.5	13.1	477	1	US-08-136-922-2	Sequence 2, Appli
82	516	12.8	666	3	US-09-240-410-2	Sequence 2, Appli
83	516	12.8	666	4	US-09-689-012-2	Sequence 2, Appli
84	508	12.6	634	3	US-09-041-236-2	Sequence 2, Appli
85	508	12.6	634	4	US-09-771-467C-2	Sequence 2, Appli
86	442.5	11.0	606	3	US-09-041-236-4	Sequence 4, Appli
87	442.5	11.0	606	4	US-09-771-467C-4	Sequence 4, Appli
88	414.5	10.3	407	4	US-09-270-767-31921	Sequence 31921, A
89	414.5	10.3	407	4	US-09-270-767-47138	Sequence 47138, A
90	345.5	8.6	311	4	US-09-270-767-33444	Sequence 33444, A
91	297	7.4	57	4	US-09-578-063-24	Sequence 24, Appl
92	282.5	7.0	215	4	US-09-854-845-19	Sequence 19, Appl
93	216.5	5.4	116	4	US-09-854-845-35	Sequence 35, Appl
94	216	5.4	1912	4	US-09-949-016-10490	Sequence 10490, A
95	210.5	5.2	251	4	US-09-270-767-33930	Sequence 33930, A
96	210.5	5.2	265	4	US-09-270-767-31872	Sequence 31872, A
97	163	4.0	660	3	US-09-181-706-8	Sequence 8, Appli
98	163	4.0	660	3	US-09-458-791-8	Sequence 8, Appli
99	163	4.0	660	3	US-09-459-066-8	Sequence 8, Appli
100	163	4.0	660	4	US-09-459-065-8	Sequence 8, Appli
101	156	3.9	31	4	US-09-578-063-20	Sequence 20, Appl
102	151.5	3.8	1568	3	US-09-181-706-2	Sequence 2, Appli
103	151.5	3.8	1568	3	US-09-458-791-2	Sequence 2, Appli
104	151.5	3.8	1568	3	US-09-459-066-2	Sequence 2, Appli
105	151.5	3.8	1568	4	US-09-459-065-2	Sequence 2, Appli
106	151.5	3.8	1651	4	US-09-949-016-10643	Sequence 10643, A
107	149.5	3.7	90	4	US-09-513-999C-4496	Sequence 4496, Ap
108	145	3.6	441	1	US-08-121-713D-56	Sequence 56, Appl
109	145	3.6	441	1	US-08-835-268-56	Sequence 56, Appl
110	145	3.6	441	2	US-09-060-692-56	Sequence 56, Appl
111	145	3.6	441	3	US-08-833-391-56	Sequence 56, Appl
112	145	3.6	441	3	US-09-060-610-56	Sequence 56, Appl
113	145	3.6	441	5	PCT-US94-10151A-56	Sequence 56, Appl
114	145	3.6	552	4	US-09-907-794A-170	Sequence 170, App
115	145	3.6	552	4	US-09-905-125A-170	Sequence 170, App
116	145	3.6	552	4	US-09-902-775A-170	Sequence 170, App
117	145	3.6	552	4	US-09-906-700-170	Sequence 170, App
118	145	3.6	552	4	US-09-903-603A-170	Sequence 170, App
119	145	3.6	552	4	US-09-904-920A-170	Sequence 170, App
120	145	3.6	552	4	US-09-909-064-170	Sequence 170, App
121	145	3.6	552	4	US-09-905-381A-170	Sequence 170, App
122	145	3.6	552	4	US-09-906-618-170	Sequence 170, App
123	130	3.2	215	3	US-09-240-410-4	Sequence 4, Appli
124	118	2.9	1665	4	US-09-858-664A-2	Sequence 2, Appli
125	118	2.9	1665	4	US-10-274-978-2	Sequence 2, Appli

126	118	2.9	1665	4	US-10-697-263-2	Sequence 2, Appli
127	114	2.8	3567	2	US-07-642-734C-4	Sequence 4, Appli
128	114	2.8	3567	3	US-08-439-009A-4	Sequence 4, Appli
129	111	2.8	4928	3	US-09-036-987A-5	Sequence 5, Appli
130	111	2.8	4928	3	US-09-370-700-5	Sequence 5, Appli
131	111	2.8	4928	4	US-09-603-207-5	Sequence 5, Appli
132	108.5	2.7	119	4	US-09-513-999C-4613	Sequence 4613, Ap
133	107.5	2.7	800	4	US-09-252-991A-21975	Sequence 21975, A
134	106.5	2.6	591	3	US-09-352-159-46	Sequence 46, Appl
135	106.5	2.6	591	4	US-09-771-045B-46	Sequence 46, Appl
136	106	2.6	3519	3	US-09-428-517-4	Sequence 4, Appli
137	105.5	2.6	3816	3	US-09-428-517-3	Sequence 3, Appli
138	102.5	2.5	657	3	US-08-508-761B-2	Sequence 2, Appli
139	102.5	2.5	1404	4	US-09-345-473E-24	Sequence 24, Appl
140	101.5	2.5	1224	4	US-09-902-540-16312	Sequence 16312, A
141	100.5	2.5	950	3	US-09-449-285A-4	Sequence 4, Appli
142	99.5	2.5	3218	1	US-08-764-100-27	Sequence 27, Appl
143	99.5	2.5	4150	3	US-09-428-517-2	Sequence 2, Appli
144	99	2.5	3038	1	US-08-450-332-2	Sequence 2, Appli
145	99	2.5	3038	2	US-08-637-640-2	Sequence 2, Appli
146	99	2.5	3038	3	US-09-004-406C-2	Sequence 2, Appli
147	99	2.5	6095	3	US-09-144-085-2	Sequence 2, Appli
148	97.5	2.4	865	4	US-09-751-687-16	Sequence 16, Appl
149	97.5	2.4	6396	4	US-09-410-551B-72	Sequence 72, Appl
150	97.5	2.4	6396	4	US-09-940-316B-72	Sequence 72, Appl
151	97	2.4	590	4	US-09-594-506-41	Sequence 41, Appl
152	97	2.4	610	4	US-09-455-777-2	Sequence 2, Appli
153	97	2.4	857	4	US-09-751-687-17	Sequence 17, Appl
154	97	2.4	1050	3	US-09-045-632-49	Sequence 49, Appl
155	97	2.4	1618	3	US-08-462-467B-4	Sequence 4, Appli
156	97	2.4	1621	1	US-08-242-677-2	Sequence 2, Appli
157	97	2.4	2887	3	US-08-462-467B-2	Sequence 2, Appli
158	96.5	2.4	1024	4	US-09-562-737-46	Sequence 46, Appl
159	96	2.4	605	3	US-09-063-950-5	Sequence 5, Appli
160	96	2.4	876	4	US-09-902-540-12110	Sequence 12110, A
161	96	2.4	1050	3	US-09-045-632-50	Sequence 50, Appl
162	96	2.4	3562	4	US-09-679-279-14	Sequence 14, Appl
163	96	2.4	3724	2	US-08-804-227C-10	Sequence 10, Appl
164	96	2.4	3724	2	US-08-804-198-4	Sequence 4, Appli
165	95.5	2.4	1000	3	US-09-352-159-25	Sequence 25, Appl
166	95.5	2.4	1000	3	US-09-352-168-25	Sequence 25, Appl
167	95.5	2.4	1000	4	US-09-771-045B-25	Sequence 25, Appl
168	95.5	2.4	1000	4	US-09-770-564A-25	Sequence 25, Appl
169	95.5	2.4	1205	3	US-09-352-159-29	Sequence 29, Appl
170	95.5	2.4	1205	3	US-09-352-168-29	Sequence 29, Appl
171	95.5	2.4	1205	4	US-09-771-045B-29	Sequence 29, Appl
172	95.5	2.4	1205	4	US-09-770-564A-29	Sequence 29, Appl
173	95	2.4	953	4	US-09-845-583A-4	Sequence 4, Appli
174	95	2.4	4391	4	US-10-006-011A-2	Sequence 2, Appli
175	94.5	2.3	1345	4	US-09-949-016-8313	Sequence 8313, Ap
176	94.5	2.3	1741	4	US-09-902-540-11253	Sequence 11253, A
177	94.5	2.3	2214	1	US-08-727-034-7	Sequence 7, Appli
178	94.5	2.3	2214	4	US-09-919-039-40	Sequence 40, Appl
179	94.5	2.3	2595	3	US-09-036-987A-2	Sequence 2, Appli
180	94.5	2.3	2595	3	US-09-370-700-2	Sequence 2, Appli
181	94.5	2.3	2595	4	US-09-603-207-2	Sequence 2, Appli
182	94	2.3	2629	2	US-08-751-189-4	Sequence 4, Appli

183	94	2.3	2629	2	US-09-060-836-4	Sequence 4, Appli
184	94	2.3	2629	3	US-09-184-445-4	Sequence 4, Appli
185	93.5	2.3	396	4	US-09-252-991A-18959	Sequence 18959, A
186	93.5	2.3	600	4	US-09-882-694B-31	Sequence 31, Appl
187	93.5	2.3	600	4	US-09-882-694B-33	Sequence 33, Appl
188	93	2.3	556	3	US-08-462-467B-24	Sequence 24, Appl
189	93	2.3	580	4	US-09-949-016-10022	Sequence 10022, A
190	93	2.3	2451	4	US-09-949-016-9675	Sequence 9675, Ap
191	93	2.3	2887	3	US-08-462-467B-8	Sequence 8, Appli
192	92.5	2.3	431	3	US-08-985-950-14	Sequence 14, Appl
193	92.5	2.3	431	3	US-08-985-950-20	Sequence 20, Appl
194	92.5	2.3	431	4	US-09-546-049-14	Sequence 14, Appl
195	92.5	2.3	431	4	US-09-546-049-20	Sequence 20, Appl
196	92.5	2.3	631	4	US-09-134-000C-6175	Sequence 6175, Ap
197	92.5	2.3	888	4	US-09-697-022-4	Sequence 4, Appli
198	92.5	2.3	888	4	US-09-697-022-5	Sequence 5, Appli
199	92.5	2.3	1479	3	US-08-840-062-2	Sequence 2, Appli
200	92	2.3	21	4	US-09-578-063-23	Sequence 23, Appl
201	92	2.3	598	3	US-09-310-463-10	Sequence 10, Appl
202	92	2.3	598	4	US-08-842-248A-10	Sequence 10, Appl
203	92	2.3	615	3	US-08-985-950-16	Sequence 16, Appl
204	92	2.3	615	3	US-08-985-950-18	Sequence 18, Appl
205	92	2.3	615	4	US-09-546-049-16	Sequence 16, Appl
206	92	2.3	615	4	US-09-546-049-18	Sequence 18, Appl
207	91.5	2.3	173	3	US-09-134-001C-5264	Sequence 5264, Ap
208	91	2.3	1620	1	US-08-542-363-2	Sequence 2, Appli
209	91	2.3	1620	3	US-09-100-089-2	Sequence 2, Appli
210	91	2.3	1620	4	US-09-670-827-2	Sequence 2, Appli
211	91	2.3	1620	4	US-09-827-949-2	Sequence 2, Appli
212	91	2.3	2588	3	US-08-936-135-2	Sequence 2, Appli
213	90.5	2.2	308	4	US-09-252-991A-18097	Sequence 18097, A
214	90.5	2.2	352	4	US-09-949-016-11359	Sequence 11359, A
215	90.5	2.2	457	1	US-08-416-478A-8	Sequence 8, Appli
216	90.5	2.2	457	2	US-08-474-988B-8	Sequence 8, Appli
217	90.5	2.2	457	2	US-08-394-442B-8	Sequence 8, Appli
218	90.5	2.2	522	3	US-08-821-984-10	Sequence 10, Appl
219	90.5	2.2	522	3	US-09-329-749-10	Sequence 10, Appl
220	90.5	2.2	522	4	US-09-502-264-10	Sequence 10, Appl
221	90.5	2.2	552	4	US-09-489-039A-13735	Sequence 13735, A
222	90.5	2.2	688	4	US-09-949-016-11400	Sequence 11400, A
223	90.5	2.2	1543	4	US-09-902-540-15547	Sequence 15547, A
224	90	2.2	540	4	US-09-949-016-11511	Sequence 11511, A
225	90	2.2	556	3	US-08-462-467B-26	Sequence 26, Appl
226	90	2.2	734	4	US-09-949-016-10597	Sequence 10597, A
227	90	2.2	1192	4	US-09-902-540-12662	Sequence 12662, A
228	90	2.2	4545	2	US-08-804-227C-14	Sequence 14, Appl
229	90	2.2	4550	2	US-08-804-227C-8	Sequence 8, Appli
230	90	2.2	4550	2	US-08-804-198-2	Sequence 2, Appli
231	89.5	2.2	470	4	US-09-949-016-10559	Sequence 10559, A
232	89.5	2.2	530	4	US-09-949-016-9519	Sequence 9519, Ap
233	89.5	2.2	947	3	US-09-228-986-73	Sequence 73, Appl
234	89.5	2.2	947	4	US-10-101-464A-73	Sequence 73, Appl
235	89.5	2.2	1463	4	US-09-949-016-11696	Sequence 11696, A
236	89.5	2.2	1464	3	US-08-891-640-2	Sequence 2, Appli
237	89.5	2.2	1464	4	US-09-949-016-6738	Sequence 6738, Ap
238	89.5	2.2	2618	3	US-09-413-814-28	Sequence 28, Appl
239	89	2.2	126	4	US-09-252-991A-28364	Sequence 28364, A

240	89	2.2	452	2	US-08-343-443B-4	Sequence 4, Appli
241	89	2.2	525	3	US-09-369-364A-21	Sequence 21, Appl
242	89	2.2	553	3	US-09-413-814-3	Sequence 3, Appli
243	88.5	2.2	539	2	US-08-808-931-16	Sequence 16, Appl
244	88.5	2.2	539	3	US-08-808-323-16	Sequence 16, Appl
245	88.5	2.2	539	3	US-09-050-603A-16	Sequence 16, Appl
246	88.5	2.2	539	3	US-09-102-420B-16	Sequence 16, Appl
247	88.5	2.2	539	3	US-09-497-698-16	Sequence 16, Appl
248	88.5	2.2	539	4	US-09-730-525-16	Sequence 16, Appl
249	88.5	2.2	839	4	US-09-751-687-15	Sequence 15, Appl
250	88.5	2.2	1198	3	US-09-199-637A-405	Sequence 405, App
251	88.5	2.2	1536	3	US-09-413-814-10	Sequence 10, Appl
252	88.5	2.2	4968	4	US-09-424-783-5	Sequence 5, Appli
253	88	2.2	412	4	US-09-252-991A-18174	Sequence 18174, A
254	88	2.2	428	4	US-09-949-016-6640	Sequence 6640, Ap
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256	88	2.2	1421	3	US-09-335-409-2	Sequence 2, Appli
257	88	2.2	1421	3	US-09-568-102-2	Sequence 2, Appli
258	88	2.2	1421	3	US-09-567-969-2	Sequence 2, Appli
259	88	2.2	1421	3	US-09-568-480-2	Sequence 2, Appli
260	88	2.2	1421	3	US-09-568-486-2	Sequence 2, Appli
261	88	2.2	1421	3	US-09-568-472-2	Sequence 2, Appli
262	88	2.2	1421	3	US-09-567-899-2	Sequence 2, Appli
263	88	2.2	1548	3	US-09-376-330-15	Sequence 15, Appl
264	88	2.2	4861	4	US-09-919-497-70	Sequence 70, Appl
265	87.5	2.2	417	3	US-08-462-467B-6	Sequence 6, Appli
266	87.5	2.2	417	3	US-08-462-467B-10	Sequence 10, Appl
267	87.5	2.2	422	4	US-09-427-501-2	Sequence 2, Appli
268	87.5	2.2	422	4	US-09-905-119A-2	Sequence 2, Appli
269	87.5	2.2	438	4	US-09-198-452A-777	Sequence 777, App
270	87.5	2.2	438	4	US-09-438-185A-731	Sequence 731, App
271	87.5	2.2	464	4	US-09-252-991A-27367	Sequence 27367, A
272	87.5	2.2	814	4	US-09-252-991A-22923	Sequence 22923, A
273	87	2.2	476	4	US-09-724-797-88	Sequence 88, Appl
274	87	2.2	712	1	US-08-587-889-2	Sequence 2, Appli
275	87	2.2	712	2	US-08-980-060-5	Sequence 5, Appli
276	87	2.2	712	3	US-09-307-185-5	Sequence 5, Appli
277	87	2.2	712	4	US-09-773-753-5	Sequence 5, Appli
278	87	2.2	712	5	PCT-US96-09193-2	Sequence 2, Appli
279	87	2.2	1481	2	US-08-616-844-40	Sequence 40, Appl
280	87	2.2	1481	2	US-08-599-654-40	Sequence 40, Appl
281	87	2.2	1481	3	US-08-944-868A-40	Sequence 40, Appl
282	87	2.2	1481	3	US-08-944-423A-40	Sequence 40, Appl
283	87	2.2	1481	3	US-08-944-496-40	Sequence 40, Appl
284	87	2.2	1882	3	US-09-369-364A-13	Sequence 13, Appl
285	86.5	2.1	349	4	US-09-919-497-76	Sequence 76, Appl
286	86.5	2.1	361	4	US-09-902-540-10811	Sequence 10811, A
287	86.5	2.1	467	4	US-09-489-039A-12308	Sequence 12308, A
288	86.5	2.1	514	4	US-09-134-000C-5666	Sequence 5666, Ap
289	86.5	2.1	600	4	US-09-882-694B-29	Sequence 29, Appl
290	86.5	2.1	967	4	US-09-130-491-2	Sequence 2, Appli
291	86.5	2.1	1081	3	US-09-369-364A-17	Sequence 17, Appl
292	86.5	2.1	3635	4	US-09-845-583A-2	Sequence 2, Appli
293	86	2.1	399	3	US-09-252-292C-24	Sequence 24, Appl
294	86	2.1	399	4	US-09-153-599A-9	Sequence 9, Appli
295	86	2.1	399	4	US-09-567-615B-13	Sequence 13, Appl
296	86	2.1	625	4	US-09-902-540-12183	Sequence 12183, A

297	86	2.1	724	4	US-09-252-991A-30228	Sequence 30228, A
298	86	2.1	756	4	US-09-937-521-13	Sequence 13, Appl
299	86	2.1	1205	2	US-08-319-866-10	Sequence 10, Appl
300	86	2.1	1205	3	US-09-123-708-6	Sequence 6, Appli
301	86	2.1	1205	3	US-09-123-624-6	Sequence 6, Appli
302	86	2.1	1205	4	US-08-809-917-10	Sequence 10, Appl
303	86	2.1	1376	4	US-09-252-991A-29515	Sequence 29515, A
304	86	2.1	1439	2	US-08-449-644-2	Sequence 2, Appli
305	86	2.1	1439	2	US-08-087-244A-2	Sequence 2, Appli
306	86	2.1	5087	3	US-09-144-085-1	Sequence 1, Appli
307	85.5	2.1	495	4	US-09-583-110-4566	Sequence 4566, Ap
308	85.5	2.1	495	4	US-09-107-433-3388	Sequence 3388, Ap
309	85.5	2.1	576	3	US-09-367-206-23	Sequence 23, Appl
310	85.5	2.1	957	4	US-09-902-540-11082	Sequence 11082, A
311	85.5	2.1	1709	4	US-09-949-016-10503	Sequence 10503, A
312	85	2.1	461	4	US-09-902-540-16585	Sequence 16585, A
313	85	2.1	491	2	US-09-001-826-23	Sequence 23, Appl
314	85	2.1	491	4	US-09-264-854-23	Sequence 23, Appl
315	85	2.1	550	4	US-09-344-510B-4	Sequence 4, Appli
316	85	2.1	631	3	US-09-311-626B-16	Sequence 16, Appl
317	85	2.1	682	4	US-09-937-521-14	Sequence 14, Appl
318	85	2.1	699	4	US-09-902-540-11479	Sequence 11479, A
319	85	2.1	859	4	US-09-978-522-3	Sequence 3, Appli
320	85	2.1	1020	2	US-08-070-301-3	Sequence 3, Appli
321	85	2.1	1349	4	US-08-943-144-4	Sequence 4, Appli
322	85	2.1	1455	2	US-08-726-012B-2	Sequence 2, Appli
323	85	2.1	2213	1	US-08-727-034-3	Sequence 3, Appli
324	84.5	2.1	233	3	US-08-444-644-33	Sequence 33, Appl
325	84.5	2.1	233	3	US-08-232-246A-33	Sequence 33, Appl
326	84.5	2.1	355	4	US-09-949-016-10906	Sequence 10906, A
327	84.5	2.1	506	4	US-09-902-540-15114	Sequence 15114, A
328	84.5	2.1	595	3	US-08-604-789B-3	Sequence 3, Appli
329	84.5	2.1	595	3	US-09-312-721A-3	Sequence 3, Appli
330	84.5	2.1	595	4	US-09-733-300-3	Sequence 3, Appli
331	84.5	2.1	724	4	US-09-949-016-10487	Sequence 10487, A
332	84.5	2.1	1028	4	US-09-583-110-4290	Sequence 4290, Ap
333	84.5	2.1	1030	4	US-09-107-433-2786	Sequence 2786, Ap
334	84.5	2.1	1346	3	US-09-320-878-4	Sequence 4, Appli
335	84.5	2.1	1346	3	US-09-105-537-37	Sequence 37, Appl
336	84.5	2.1	1346	4	US-09-141-908-5	Sequence 5, Appli
337	84.5	2.1	1346	4	US-09-657-440-4	Sequence 4, Appli
338	84.5	2.1	11877	3	US-09-105-537-6	Sequence 6, Appli
339	84	2.1	263	2	US-08-206-790A-23	Sequence 23, Appl
340	84	2.1	263	4	US-09-311-784A-28	Sequence 28, Appl
341	84	2.1	263	4	US-09-949-016-6175	Sequence 6175, Ap
342	84	2.1	263	5	PCT-US95-02943-23	Sequence 23, Appl
343	84	2.1	272	4	US-09-949-016-11564	Sequence 11564, A
344	84	2.1	314	4	US-09-489-039A-8342	Sequence 8342, Ap
345	84	2.1	379	4	US-09-079-030-81	Sequence 81, Appl
346	84	2.1	415	4	US-09-107-532A-6491	Sequence 6491, Ap
347	84	2.1	436	4	US-09-949-016-7854	Sequence 7854, Ap
348	84	2.1	538	3	US-09-175-928-4	Sequence 4, Appli
349	84	2.1	588	1	US-08-391-615-5	Sequence 5, Appli
350	84	2.1	675	4	US-09-902-540-12713	Sequence 12713, A
351	84	2.1	695	3	US-09-314-242-12	Sequence 12, Appl
352	84	2.1	726	3	US-09-413-814-30	Sequence 30, Appl
353	84	2.1	841	4	US-09-902-540-14896	Sequence 14896, A

354	84	2.1	843	4	US-08-591-502B-53	Sequence 53, Appl
355	84	2.1	843	4	US-08-591-502B-59	Sequence 59, Appl
356	84	2.1	862	4	US-09-978-522-1	Sequence 1, Appli
357	84	2.1	922	4	US-09-883-134-9	Sequence 9, Appli
358	84	2.1	1014	4	US-09-344-510B-3	Sequence 3, Appli
359	84	2.1	2627	2	US-08-751-189-3	Sequence 3, Appli
360	84	2.1	2627	2	US-09-060-836-3	Sequence 3, Appli
361	84	2.1	2627	3	US-09-184-445-3	Sequence 3, Appli
362	84	2.1	2972	4	US-08-469-260A-387	Sequence 387, App
363	84	2.1	2972	4	US-08-488-446-387	Sequence 387, App
364	84	2.1	2972	4	US-08-467-344A-387	Sequence 387, App
365	84	2.1	2972	4	US-08-424-550B-387	Sequence 387, App
366	84	2.1	3623	4	US-09-341-461-2	Sequence 2, Appli
367	84	2.1	3647	4	US-09-949-016-10932	Sequence 10932, A
368	83.5	2.1	172	4	US-09-902-540-11689	Sequence 11689, A
369	83.5	2.1	281	4	US-09-270-767-42623	Sequence 42623, A
370	83.5	2.1	469	1	US-08-363-215-1	Sequence 1, Appli
371	83.5	2.1	469	3	US-08-807-342B-6	Sequence 6, Appli
372	83.5	2.1	480	2	US-08-895-521-4	Sequence 4, Appli
373	83.5	2.1	480	3	US-09-235-218-4	Sequence 4, Appli
374	83.5	2.1	490	4	US-09-252-991A-30355	Sequence 30355, A
375	83.5	2.1	549	4	US-09-949-016-10821	Sequence 10821, A
376	83.5	2.1	576	3	US-09-367-206-22	Sequence 22, Appl
377	83.5	2.1	587	3	US-09-102-528-30	Sequence 30, Appl
378	83.5	2.1	595	2	US-08-232-087A-2	Sequence 2, Appli
379	83.5	2.1	595	3	US-09-006-353A-9	Sequence 9, Appli
380	83.5	2.1	595	4	US-09-573-986-9	Sequence 9, Appli
381	83.5	2.1	595	4	US-09-949-016-6048	Sequence 6048, Ap
382	83.5	2.1	598	3	US-09-352-159-42	Sequence 42, Appl
383	83.5	2.1	598	4	US-09-771-045B-42	Sequence 42, Appl
384	83.5	2.1	618	4	US-09-970-516-4	Sequence 4, Appli
385	83.5	2.1	618	4	US-09-817-676A-14	Sequence 14, Appl
386	83.5	2.1	640	4	US-09-177-165A-30	Sequence 30, Appl
387	83.5	2.1	642	4	US-09-949-016-8043	Sequence 8043, Ap
388	83.5	2.1	780	4	US-09-902-540-13911	Sequence 13911, A
389	83.5	2.1	841	4	US-09-949-016-9669	Sequence 9669, Ap
390	83.5	2.1	1040	3	US-09-564-805-238	Sequence 238, App
391	83.5	2.1	1317	3	US-09-083-521-7	Sequence 7, Appli
392	83.5	2.1	1385	4	US-09-827-998-16	Sequence 16, Appl
393	83.5	2.1	1963	4	US-09-949-016-8888	Sequence 8888, Ap
394	83	2.1	303	4	US-09-739-455-12	Sequence 12, Appl
395	83	2.1	303	4	US-09-739-455-22	Sequence 22, Appl
396	83	2.1	304	4	US-09-543-681A-7290	Sequence 7290, Ap
397	83	2.1	308	4	US-09-599-360B-91	Sequence 91, Appl
398	83	2.1	308	4	US-09-599-361-2	Sequence 2, Appli
399	83	2.1	348	3	US-08-652-265-2	Sequence 2, Appli
400	83	2.1	348	3	US-08-652-265-6	Sequence 6, Appli
401	83	2.1	348	3	US-08-834-497A-2	Sequence 2, Appli
402	83	2.1	348	3	US-08-834-497A-6	Sequence 6, Appli
403	83	2.1	348	3	US-09-503-444A-2	Sequence 2, Appli
404	83	2.1	348	3	US-09-503-444A-6	Sequence 6, Appli
405	83	2.1	348	3	US-09-277-457-2	Sequence 2, Appli
406	83	2.1	348	4	US-09-679-729-2	Sequence 2, Appli
407	83	2.1	348	4	US-09-949-016-5935	Sequence 5935, Ap
408	83	2.1	357	4	US-09-949-016-7051	Sequence 7051, Ap
409	83	2.1	403	4	US-09-489-039A-11022	Sequence 11022, A
410	83	2.1	597	4	US-09-746-311B-381	Sequence 381, App

411	83	2.1	610	4	US-09-328-352-7804	Sequence 7804, Ap
412	83	2.1	648	4	US-09-902-540-14001	Sequence 14001, A
413	83	2.1	650	3	US-09-310-463-2	Sequence 2, Appli
414	83	2.1	650	4	US-08-842-248A-2	Sequence 2, Appli
415	83	2.1	651	3	US-08-985-950-22	Sequence 22, Appl
416	83	2.1	651	4	US-09-546-049-22	Sequence 22, Appl
417	83	2.1	864	4	US-09-751-687-18	Sequence 18, Appl
418	83	2.1	974	4	US-09-883-134-7	Sequence 7, Appli
419	83	2.1	1269	4	US-09-902-540-10352	Sequence 10352, A
420	83	2.1	1375	3	US-09-210-361-4	Sequence 4, Appli
421	83	2.1	1375	4	US-09-740-274-4	Sequence 4, Appli
422	82.5	2.0	215	4	US-09-252-991A-20040	Sequence 20040, A
423	82.5	2.0	576	3	US-09-367-206-1	Sequence 1, Appli
424	82.5	2.0	576	3	US-09-367-206-21	Sequence 21, Appl
425	82.5	2.0	595	1	US-08-225-989-2	Sequence 2, Appli
426	82.5	2.0	595	1	US-08-570-923-2	Sequence 2, Appli
427	82.5	2.0	595	1	US-08-580-014-2	Sequence 2, Appli
428	82.5	2.0	595	3	US-09-079-785-2	Sequence 2, Appli
429	82.5	2.0	595	4	US-09-921-667-6	Sequence 6, Appli
430	82.5	2.0	595	4	US-09-628-126-2	Sequence 2, Appli
431	82.5	2.0	607	2	US-08-878-989-15	Sequence 15, Appl
432	82.5	2.0	607	3	US-09-272-796-15	Sequence 15, Appl
433	82.5	2.0	632	4	US-09-634-238-249	Sequence 249, App
434	82.5	2.0	648	2	US-08-817-436A-2	Sequence 2, Appli
435	82.5	2.0	1193	4	US-09-949-016-10498	Sequence 10498, A
436	82.5	2.0	1198	4	US-09-949-016-6989	Sequence 6989, Ap
437	82.5	2.0	1203	4	US-09-949-016-10916	Sequence 10916, A
438	82.5	2.0	1350	3	US-09-245-041-17	Sequence 17, Appl
439	82.5	2.0	1350	4	US-09-358-055B-17	Sequence 17, Appl
440	82.5	2.0	1350	4	US-09-893-238-17	Sequence 17, Appl
441	82.5	2.0	1429	3	US-09-245-041-130	Sequence 130, App
442	82.5	2.0	1429	4	US-09-358-055B-131	Sequence 131, App
443	82.5	2.0	2109	3	US-08-646-695-6	Sequence 6, Appli
444	82.5	2.0	2109	5	PCT-US96-06053-6	Sequence 6, Appli
445	82.5	2.0	2787	3	US-09-245-041-15	Sequence 15, Appl
446	82.5	2.0	2787	4	US-09-358-055B-15	Sequence 15, Appl
447	82.5	2.0	2787	4	US-09-893-238-15	Sequence 15, Appl
448	82	2.0	396	4	US-09-543-681A-5161	Sequence 5161, Ap
449	82	2.0	417	4	US-09-538-092-424	Sequence 424, App
450	82	2.0	432	2	US-09-099-677A-3	Sequence 3, Appli
451	82	2.0	432	3	US-09-261-471-3	Sequence 3, Appli
452	82	2.0	570	4	US-09-248-796A-15079	Sequence 15079, A
453	82	2.0	591	3	US-09-352-159-44	Sequence 44, Appl
454	82	2.0	591	4	US-09-771-045B-44	Sequence 44, Appl
455	82	2.0	855	2	US-08-482-090-12	Sequence 12, Appl
456	82	2.0	856	2	US-08-481-700B-8	Sequence 8, Appli
457	82	2.0	856	2	US-09-007-383-16	Sequence 16, Appl
458	82	2.0	977	3	US-09-302-812-2	Sequence 2, Appli
459	82	2.0	977	3	US-09-511-477-2	Sequence 2, Appli
460	82	2.0	977	3	US-09-511-507-2	Sequence 2, Appli
461	82	2.0	1180	4	US-09-949-016-6577	Sequence 6577, Ap
462	82	2.0	1244	3	US-09-356-952-7	Sequence 7, Appli
463	82	2.0	1574	4	US-09-410-551B-25	Sequence 25, Appl
464	82	2.0	1574	4	US-09-940-316B-25	Sequence 25, Appl
465	81.5	2.0	235	3	US-08-444-644-19	Sequence 19, Appl
466	81.5	2.0	235	3	US-08-232-246A-19	Sequence 19, Appl
467	81.5	2.0	449	3	US-09-230-371A-28	Sequence 28, Appl

468	81.5	2.0	563	4	US-09-949-016-8277	Sequence 8277, Ap
469	81.5	2.0	673	3	US-09-091-725-23	Sequence 23, Appl
470	81.5	2.0	690	4	US-09-248-796A-19169	Sequence 19169, A
471	81.5	2.0	931	4	US-09-949-016-10552	Sequence 10552, A
472	81.5	2.0	1252	4	US-09-902-540-13967	Sequence 13967, A
473	81	2.0	339	1	US-08-208-007A-11	Sequence 11, Appl
474	81	2.0	339	1	US-08-330-121B-7	Sequence 7, Appli
475	81	2.0	339	3	US-08-860-255A-7	Sequence 7, Appli
476	81	2.0	339	3	US-08-915-095A-11	Sequence 11, Appl
477	81	2.0	339	3	US-08-798-096-11	Sequence 11, Appl
478	81	2.0	339	4	US-08-798-095A-11	Sequence 11, Appl
479	81	2.0	339	4	US-09-953-956-11	Sequence 11, Appl
480	81	2.0	339	4	US-08-553-125A-11	Sequence 11, Appl
481	81	2.0	339	4	US-08-536-861-7	Sequence 7, Appli
482	81	2.0	339	4	US-10-114-464-11	Sequence 11, Appl
483	81	2.0	339	4	US-09-290-586A-24	Sequence 24, Appl
484	81	2.0	339	4	US-09-949-016-6142	Sequence 6142, Ap
485	81	2.0	339	5	PCT-US95-13820-7	Sequence 7, Appli
486	81	2.0	363	4	US-09-949-016-11627	Sequence 11627, A
487	81	2.0	443	4	US-09-461-325-147	Sequence 147, App
488	81	2.0	443	4	US-10-012-542-147	Sequence 147, App
489	81	2.0	443	4	US-10-115-123-147	Sequence 147, App
490	81	2.0	604	4	US-09-489-039A-8519	Sequence 8519, Ap
491	81	2.0	979	4	US-09-538-092-482	Sequence 482, App
492	81	2.0	1130	4	US-09-976-594-280	Sequence 280, App
493	81	2.0	2141	4	US-09-949-016-10918	Sequence 10918, A
494	81	2.0	4302	3	US-09-052-469-8	Sequence 8, Appli
495	81	2.0	4302	4	US-08-422-582-8	Sequence 8, Appli
496	81	2.0	4302	4	US-09-052-262-8	Sequence 8, Appli
497	81	2.0	4339	3	US-09-052-469-6	Sequence 6, Appli
498	81	2.0	4339	4	US-08-422-582-6	Sequence 6, Appli
499	81	2.0	4339	4	US-09-052-262-6	Sequence 6, Appli
500	80.5	2.0	363	4	US-09-252-991A-26018	Sequence 26018, A
501	80.5	2.0	408	4	US-09-489-039A-10513	Sequence 10513, A
502	80.5	2.0	417	4	US-09-820-002-4	Sequence 4, Appli
503	80.5	2.0	456	4	US-09-248-796A-19808	Sequence 19808, A
504	80.5	2.0	460	4	US-09-813-453B-39	Sequence 39, Appl
505	80.5	2.0	470	4	US-09-252-991A-23310	Sequence 23310, A
506	80.5	2.0	502	4	US-09-248-796A-15922	Sequence 15922, A
507	80.5	2.0	720	4	US-09-604-605-2	Sequence 2, Appli
508	80.5	2.0	760	4	US-09-252-991A-18711	Sequence 18711, A
509	80.5	2.0	857	4	US-09-902-540-12028	Sequence 12028, A
510	80.5	2.0	977	4	US-09-252-991A-28261	Sequence 28261, A
511	80.5	2.0	1191	4	US-09-540-236-2902	Sequence 2902, Ap
512	80.5	2.0	1205	1	US-07-908-245-2	Sequence 2, Appli
513	80.5	2.0	1260	3	US-09-245-041-2	Sequence 2, Appli
514	80.5	2.0	1260	4	US-09-358-055B-2	Sequence 2, Appli
515	80.5	2.0	1260	4	US-09-893-238-2	Sequence 2, Appli
516	80.5	2.0	1323	3	US-09-770-170-2	Sequence 2, Appli
517	80.5	2.0	1637	3	US-09-718-692-2	Sequence 2, Appli
518	80.5	2.0	1637	4	US-09-718-852-2	Sequence 2, Appli
519	80.5	2.0	1637	4	US-09-718-815-2	Sequence 2, Appli
520	80.5	2.0	1843	3	US-09-413-814-50	Sequence 50, Appl
521	80	2.0	281	4	US-09-949-016-8447	Sequence 8447, Ap
522	80	2.0	340	4	US-09-902-540-11600	Sequence 11600, A
523	80	2.0	362	4	US-09-252-991A-18068	Sequence 18068, A
524	80	2.0	380	3	US-08-307-896-1	Sequence 1, Appli

525	80	2.0	380	4	US-09-949-016-9251	Sequence 9251, Ap
526	80	2.0	394	4	US-09-442-349A-106	Sequence 106, App
527	80	2.0	394	4	US-09-963-137-192	Sequence 192, App
528	80	2.0	394	4	US-09-963-137-194	Sequence 194, App
529	80	2.0	394	5	PCT-US95-11808-1	Sequence 1, Appli
530	80	2.0	489	3	US-09-310-463-14	Sequence 14, Appl
531	80	2.0	489	4	US-08-842-248A-14	Sequence 14, Appl
532	80	2.0	489	4	US-09-949-016-6765	Sequence 6765, Ap
533	80	2.0	495	3	US-08-962-859A-2	Sequence 2, Appli
534	80	2.0	510	4	US-09-949-016-10733	Sequence 10733, A
535	80	2.0	523	4	US-09-549-519-35	Sequence 35, Appl
536	80	2.0	523	4	US-09-549-519-36	Sequence 36, Appl
537	80	2.0	532	4	US-09-489-039A-9142	Sequence 9142, Ap
538	80	2.0	756	4	US-09-438-268-4	Sequence 4, Appli
539	80	2.0	756	4	US-09-963-137-184	Sequence 184, App
540	80	2.0	775	4	US-09-513-838-6	Sequence 6, Appli
541	80	2.0	781	4	US-09-949-016-9170	Sequence 9170, Ap
542	80	2.0	842	4	US-08-591-502B-51	Sequence 51, Appl
543	80	2.0	946	4	US-09-902-540-16817	Sequence 16817, A
544	80	2.0	991	4	US-09-902-540-11984	Sequence 11984, A
545	80	2.0	1047	4	US-09-529-239D-99	Sequence 99, Appl
546	80	2.0	1051	4	US-09-252-991A-25232	Sequence 25232, A
547	80	2.0	1113	4	US-09-270-767-42704	Sequence 42704, A
548	80	2.0	1155	4	US-09-949-016-9550	Sequence 9550, Ap
549	80	2.0	1181	4	US-09-826-509-587	Sequence 587, App
550	80	2.0	1248	4	US-10-042-810-2	Sequence 2, Appli
551	80	2.0	1278	4	US-10-042-810-4	Sequence 4, Appli
552	80	2.0	1334	6	5476657-1	Patent No. 5476657
553	80	2.0	1334	6	5476657-1	Patent No. 5476657
554	80	2.0	1338	4	US-09-631-603-2	Sequence 2, Appli
555	80	2.0	1441	4	US-09-949-016-10397	Sequence 10397, A
556	80	2.0	1475	3	US-09-007-999-2	Sequence 2, Appli
557	80	2.0	1475	3	US-09-210-361-2	Sequence 2, Appli
558	80	2.0	1475	4	US-09-740-274-2	Sequence 2, Appli
559	80	2.0	1485	4	US-08-851-567B-32	Sequence 32, Appl
560	80	2.0	1770	4	US-09-827-998-10	Sequence 10, Appl
561	80	2.0	1791	4	US-09-827-998-3	Sequence 3, Appli
562	80	2.0	1799	4	US-09-134-000C-5178	Sequence 5178, Ap
563	80	2.0	2362	4	US-09-949-016-8985	Sequence 8985, Ap
564	80	2.0	4544	1	US-08-469-486-52	Sequence 52, Appl
565	80	2.0	4544	2	US-08-469-658-52	Sequence 52, Appl
566	79.5	2.0	178	4	US-09-252-991A-31841	Sequence 31841, A
567	79.5	2.0	205	4	US-08-134-231C-25	Sequence 25, Appl
568	79.5	2.0	205	4	US-08-728-160-25	Sequence 25, Appl
569	79.5	2.0	228	4	US-09-270-767-44420	Sequence 44420, A
570	79.5	2.0	313	3	US-08-985-335-8	Sequence 8, Appli
571	79.5	2.0	313	3	US-09-410-372-8	Sequence 8, Appli
572	79.5	2.0	330	4	US-09-489-039A-11749	Sequence 11749, A
573	79.5	2.0	369	4	US-09-270-767-46150	Sequence 46150, A
574	79.5	2.0	416	4	US-09-902-540-14976	Sequence 14976, A
575	79.5	2.0	557	4	US-09-489-039A-13795	Sequence 13795, A
576	79.5	2.0	616	4	US-09-252-991A-25638	Sequence 25638, A
577	79.5	2.0	672	4	US-09-252-991A-25389	Sequence 25389, A
578	79.5	2.0	776	4	US-09-523-849-34	Sequence 34, Appl
579	79.5	2.0	854	2	US-08-456-647B-20	Sequence 20, Appl
580	79.5	2.0	854	2	US-08-237-401A-20	Sequence 20, Appl
581	79.5	2.0	863	1	US-08-325-547-4	Sequence 4, Appli

582	79.5	2.0	1024	4	US-09-562-737-41	Sequence 41, Appl
583	79.5	2.0	1129	4	US-09-489-039A-10200	Sequence 10200, A
584	79.5	2.0	1235	4	US-09-949-016-8455	Sequence 8455, Ap
585	79.5	2.0	1235	4	US-09-949-016-8456	Sequence 8456, Ap
586	79.5	2.0	1298	4	US-09-252-991A-30579	Sequence 30579, A
587	79.5	2.0	1299	3	US-08-460-900C-62	Sequence 62, Appl
588	79.5	2.0	1299	3	US-08-674-509B-48	Sequence 48, Appl
589	79.5	2.0	1299	3	US-08-954-698-48	Sequence 48, Appl
590	79.5	2.0	1299	4	US-09-639-695-62	Sequence 62, Appl
591	79.5	2.0	1299	4	US-09-448-188-48	Sequence 48, Appl
592	79.5	2.0	1299	4	US-08-954-128-48	Sequence 48, Appl
593	79.5	2.0	1299	4	US-08-954-740-48	Sequence 48, Appl
594	79.5	2.0	1517	4	US-09-410-551B-19	Sequence 19, Appl
595	79.5	2.0	1517	4	US-09-940-316B-19	Sequence 19, Appl
596	79.5	2.0	3854	4	US-09-949-016-7876	Sequence 7876, Ap
597	79.5	2.0	4630	4	US-09-091-609-2	Sequence 2, Appli
598	79.5	2.0	5215	3	US-09-105-537-2	Sequence 2, Appli
599	79.5	2.0	7257	3	US-09-335-409-5	Sequence 5, Appli
600	79.5	2.0	7257	3	US-09-568-102-5	Sequence 5, Appli
601	79.5	2.0	7257	3	US-09-567-969-5	Sequence 5, Appli
602	79.5	2.0	7257	3	US-09-568-480-5	Sequence 5, Appli
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604	79.5	2.0	7257	3	US-09-568-472-5	Sequence 5, Appli
605	79.5	2.0	7257	3	US-09-567-899-5	Sequence 5, Appli
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608	79	2.0	353	4	US-09-828-302-14	Sequence 14, Appl
609	79	2.0	396	3	US-08-985-908-24	Sequence 24, Appl
610	79	2.0	416	4	US-09-270-767-41063	Sequence 41063, A
611	79	2.0	416	4	US-09-270-767-56279	Sequence 56279, A
612	79	2.0	447	4	US-09-746-311B-379	Sequence 379, App
613	79	2.0	448	3	US-09-310-463-18	Sequence 18, Appl
614	79	2.0	448	4	US-08-842-248A-18	Sequence 18, Appl
615	79	2.0	448	4	US-09-949-016-6764	Sequence 6764, Ap
616	79	2.0	449	3	US-09-310-463-38	Sequence 38, Appl
617	79	2.0	452	4	US-09-949-016-7182	Sequence 7182, Ap
618	79	2.0	455	4	US-09-949-016-7116	Sequence 7116, Ap
619	79	2.0	465	4	US-09-949-016-9259	Sequence 9259, Ap
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621	79	2.0	606	2	US-08-392-806A-6	Sequence 6, Appli
622	79	2.0	606	3	US-09-257-490-6	Sequence 6, Appli
623	79	2.0	611	4	US-09-252-991A-29866	Sequence 29866, A
624	79	2.0	798	2	US-08-222-617A-8	Sequence 8, Appli
625	79	2.0	928	1	US-08-442-248-2	Sequence 2, Appli
626	79	2.0	928	1	US-08-440-815-2	Sequence 2, Appli
627	79	2.0	928	3	US-08-486-449-2	Sequence 2, Appli
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631	79	2.0	1086	4	US-10-160-719A-38	Sequence 38, Appl
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633	79	2.0	1121	1	US-08-005-002C-2	Sequence 2, Appli
634	79	2.0	1121	1	US-08-487-203A-2	Sequence 2, Appli
635	79	2.0	1198	3	US-09-245-041-131	Sequence 131, App
636	79	2.0	1198	3	US-09-794-236-3	Sequence 3, Appli
637	79	2.0	1198	4	US-09-358-055B-132	Sequence 132, App
638	79	2.0	1745	2	US-09-031-485-33	Sequence 33, Appl

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643	79	2.0	2259	3	US-09-413-814-70	Sequence 70, Appl
644	79	2.0	2439	3	US-09-335-409-7	Sequence 7, Appli
645	79	2.0	2439	3	US-09-568-102-7	Sequence 7, Appli
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649	79	2.0	2439	3	US-09-568-472-7	Sequence 7, Appli
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655	78.5	1.9	349	3	US-09-375-419-6	Sequence 6, Appli
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678	78.5	1.9	635	4	US-09-851-847-5	Sequence 5, Appli
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694	78.5	1.9	1285	4	US-08-954-701A-6	Sequence 6, Appli
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703	78.5	1.9	1591	4	US-09-060-299-43	Sequence 43, Appl
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716	78.5	1.9	2035	5	PCT-US93-11721-5	Sequence 5, Appli
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727	78	1.9	436	4	US-09-949-016-7912	Sequence 7912, Ap
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729	78	1.9	588	3	US-09-627-216A-14	Sequence 14, Appl
730	78	1.9	588	4	US-09-765-873A-14	Sequence 14, Appl
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734	78	1.9	673	3	US-09-091-725-19	Sequence 19, Appl
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736	78	1.9	732	3	US-08-989-299-4	Sequence 4, Appli
737	78	1.9	732	4	US-09-407-427-4	Sequence 4, Appli
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766	77.5	1.9	423	3	US-09-568-486-10	Sequence 10, Appl
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779	77.5	1.9	605	4	US-09-270-767-46196	Sequence 46196, A
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784	77.5	1.9	737	4	US-09-944-457-15	Sequence 15, Appl
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787	77.5	1.9	1484	4	US-09-902-540-14332	Sequence 14332, A
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789	77.5	1.9	1588	4	US-09-410-551B-29	Sequence 29, Appl
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792	77.5	1.9	1964	3	US-09-467-997-1	Sequence 1, Appli
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795	77.5	1.9	2636	4	US-09-252-991A-25753	Sequence 25753, A
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807	77	1.9	474	4	US-09-758-124-4	Sequence 4, Appli
808	77	1.9	474	6	5395760-4	Patent No. 5395760
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814	77	1.9	549	4	US-10-274-978-6	Sequence 6, Appli
815	77	1.9	549	4	US-10-697-263-6	Sequence 6, Appli
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831	77	1.9	924	2	US-08-487-595-28	Sequence 28, Appl
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839	77	1.9	1251	4	US-09-949-016-7784	Sequence 7784, Ap
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841	77	1.9	1377	4	US-09-949-016-6058	Sequence 6058, Ap
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844	77	1.9	1403	2	US-08-535-837-3	Sequence 3, Appli
845	77	1.9	1403	3	US-09-124-491-17	Sequence 17, Appl
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850	77	1.9	4303	4	US-09-479-467A-2	Sequence 2, Appli
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865	76.5	1.9	582	4	US-09-736-457-334	Sequence 334, App
866	76.5	1.9	582	4	US-09-614-124B-334	Sequence 334, App

867	76.5	1.9	582	4	US-09-671-325-334	Sequence 334, App
868	76.5	1.9	582	4	US-09-589-184-334	Sequence 334, App
869	76.5	1.9	582	4	US-09-658-824-334	Sequence 334, App
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871	76.5	1.9	591	1	US-08-483-094-2	Sequence 2, Appli
872	76.5	1.9	600	3	US-09-352-159-36	Sequence 36, Appl
873	76.5	1.9	600	3	US-09-352-159-38	Sequence 38, Appl
874	76.5	1.9	600	4	US-09-771-045B-36	Sequence 36, Appl
875	76.5	1.9	600	4	US-09-771-045B-38	Sequence 38, Appl
876	76.5	1.9	600	4	US-09-882-694B-23	Sequence 23, Appl
877	76.5	1.9	600	4	US-09-882-694B-25	Sequence 25, Appl
878	76.5	1.9	604	4	US-09-949-016-9548	Sequence 9548, Ap
879	76.5	1.9	635	1	US-08-184-327A-4	Sequence 4, Appli
880	76.5	1.9	635	2	US-08-078-311-1	Sequence 1, Appli
881	76.5	1.9	635	2	US-08-460-402-1	Sequence 1, Appli
882	76.5	1.9	635	5	PCT-US95-00670-4	Sequence 4, Appli
883	76.5	1.9	669	4	US-09-969-532-28	Sequence 28, Appl
884	76.5	1.9	690	4	US-09-252-991A-32350	Sequence 32350, A
885	76.5	1.9	751	4	US-09-902-540-15370	Sequence 15370, A
886	76.5	1.9	782	4	US-09-252-991A-21554	Sequence 21554, A
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888	76.5	1.9	816	3	US-09-041-886-17	Sequence 17, Appl
889	76.5	1.9	816	4	US-09-538-092-1208	Sequence 1208, Ap
890	76.5	1.9	837	1	US-08-426-627-23	Sequence 23, Appl
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892	76.5	1.9	843	4	US-10-209-264-2	Sequence 2, Appli
893	76.5	1.9	900	4	US-09-969-532-12	Sequence 12, Appl
894	76.5	1.9	987	4	US-09-543-681A-7785	Sequence 7785, Ap
895	76.5	1.9	991	2	US-08-449-645A-13	Sequence 13, Appl
896	76.5	1.9	991	2	US-08-702-367A-13	Sequence 13, Appl
897	76.5	1.9	991	5	PCT-US95-04681-13	Sequence 13, Appl
898	76.5	1.9	1101	2	US-08-916-917-14	Sequence 14, Appl
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901	76.5	1.9	1307	4	US-09-252-991A-20867	Sequence 20867, A
902	76.5	1.9	1617	4	US-09-198-452A-1035	Sequence 1035, Ap
903	76.5	1.9	1617	4	US-09-438-185A-965	Sequence 965, App
904	76.5	1.9	1822	4	US-09-949-016-7999	Sequence 7999, Ap
905	76.5	1.9	2383	4	US-09-492-709A-302	Sequence 302, App
906	76.5	1.9	3892	4	US-09-328-352-5503	Sequence 5503, Ap
907	76.5	1.9	4866	4	US-09-424-783-2	Sequence 2, Appli
908	76	1.9	352	4	US-09-902-540-9921	Sequence 9921, Ap
909	76	1.9	359	4	US-09-828-523A-14	Sequence 14, Appl
910	76	1.9	370	4	US-09-828-523A-74	Sequence 74, Appl
911	76	1.9	445	4	US-09-843-905A-12	Sequence 12, Appl
912	76	1.9	467	4	US-09-902-540-11250	Sequence 11250, A
913	76	1.9	475	2	US-08-698-407-4	Sequence 4, Appli
914	76	1.9	475	3	US-09-195-855-4	Sequence 4, Appli
915	76	1.9	505	4	US-09-198-452A-1117	Sequence 1117, Ap
916	76	1.9	513	4	US-09-538-092-616	Sequence 616, App
917	76	1.9	524	4	US-09-902-540-12631	Sequence 12631, A
918	76	1.9	525	4	US-09-252-991A-23870	Sequence 23870, A
919	76	1.9	526	4	US-09-438-185A-1042	Sequence 1042, Ap
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921	76	1.9	567	3	US-08-813-150-4	Sequence 4, Appli
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923	76	1.9	597	4	US-09-902-540-11095	Sequence 11095, A

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927	76	1.9	621	2	US-08-419-652-4	Sequence 4, Appli
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929	76	1.9	639	4	US-09-782-906-2	Sequence 2, Appli
930	76	1.9	639	4	US-09-782-906-3	Sequence 3, Appli
931	76	1.9	639	4	US-09-782-906-5	Sequence 5, Appli
932	76	1.9	655	4	US-09-969-532-32	Sequence 32, Appl
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935	76	1.9	662	1	US-08-248-532-2	Sequence 2, Appli
936	76	1.9	662	2	US-08-419-652-2	Sequence 2, Appli
937	76	1.9	662	2	US-08-685-118-4	Sequence 4, Appli
938	76	1.9	662	2	US-08-915-495-4	Sequence 4, Appli
939	76	1.9	662	2	US-08-914-520-4	Sequence 4, Appli
940	76	1.9	662	3	US-08-789-350-2	Sequence 2, Appli
941	76	1.9	662	4	US-09-949-016-6624	Sequence 6624, Ap
942	76	1.9	666	4	US-09-969-532-30	Sequence 30, Appl
943	76	1.9	680	4	US-09-969-532-26	Sequence 26, Appl
944	76	1.9	680	4	US-09-734-237B-77	Sequence 77, Appl
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956	76	1.9	886	4	US-09-969-532-16	Sequence 16, Appl
957	76	1.9	897	4	US-09-969-532-14	Sequence 14, Appl
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963	76	1.9	917	2	US-08-487-595-2	Sequence 2, Appli
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967	76	1.9	1012	1	US-08-219-262B-2	Sequence 2, Appli
968	76	1.9	1012	3	US-09-031-655-2	Sequence 2, Appli
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972	76	1.9	2386	2	US-09-016-366A-12	Sequence 12, Appl
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977	75.5	1.9	231	3	US-09-182-145-97	Sequence 97, Appl
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979	75.5	1.9	233	3	US-09-182-145-95	Sequence 95, Appl
980	75.5	1.9	234	3	US-09-182-145-94	Sequence 94, Appl

981	75.5	1.9	235	3	US-09-182-145-93	Sequence 93, Appl
982	75.5	1.9	236	3	US-09-182-145-92	Sequence 92, Appl
983	75.5	1.9	237	3	US-09-182-145-91	Sequence 91, Appl
984	75.5	1.9	238	3	US-09-182-145-90	Sequence 90, Appl
985	75.5	1.9	239	3	US-09-182-145-89	Sequence 89, Appl
986	75.5	1.9	240	3	US-09-182-145-88	Sequence 88, Appl
987	75.5	1.9	241	3	US-09-182-145-87	Sequence 87, Appl
988	75.5	1.9	242	3	US-09-182-145-86	Sequence 86, Appl
989	75.5	1.9	243	3	US-09-182-145-85	Sequence 85, Appl
990	75.5	1.9	244	3	US-09-182-145-84	Sequence 84, Appl
991	75.5	1.9	245	3	US-09-182-145-83	Sequence 83, Appl
992	75.5	1.9	246	3	US-09-182-145-82	Sequence 82, Appl
993	75.5	1.9	247	3	US-09-182-145-81	Sequence 81, Appl
994	75.5	1.9	248	3	US-09-182-145-80	Sequence 80, Appl
995	75.5	1.9	249	3	US-09-182-145-79	Sequence 79, Appl
996	75.5	1.9	250	3	US-09-182-145-78	Sequence 78, Appl
997	75.5	1.9	251	3	US-09-182-145-20	Sequence 20, Appl
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1004	75.5	1.9	365	3	US-09-333-729A-3	Sequence 3, Appli
1005	75.5	1.9	397	3	US-08-978-741-6	Sequence 6, Appli
1006	75.5	1.9	397	3	US-09-333-729A-7	Sequence 7, Appli
1007	75.5	1.9	424	6	5169835-6	Patent No. 5169835
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1011	75.5	1.9	463	4	US-09-252-991A-30035	Sequence 30035, A
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1017	75.5	1.9	575	4	US-09-949-016-9760	Sequence 9760, Ap
1018	75.5	1.9	615	2	US-08-911-445-2	Sequence 2, Appli
1019	75.5	1.9	615	3	US-09-182-983-2	Sequence 2, Appli
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1027	75.5	1.9	682	3	US-09-182-983-3	Sequence 3, Appli
1028	75.5	1.9	682	4	US-09-771-838A-3	Sequence 3, Appli
1029	75.5	1.9	682	4	US-09-949-016-6591	Sequence 6591, Ap
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1031	75.5	1.9	702	3	US-09-232-197-102	Sequence 102, App
1032	75.5	1.9	702	3	US-09-232-201-102	Sequence 102, App
1033	75.5	1.9	702	4	US-09-232-195-102	Sequence 102, App
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1036	75.5	1.9	773	3	US-09-312-157-2	Sequence 2, Appli
1037	75.5	1.9	773	4	US-09-717-888-2	Sequence 2, Appli

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1042	75.5	1.9	960	4	US-09-949-016-9527	Sequence 9527, Ap
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1045	75.5	1.9	1135	3	US-09-357-014-7	Sequence 7, Appli
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1063	75	1.9	632	1	US-08-454-439-11	Sequence 11, Appl
1064	75	1.9	632	5	PCT-US94-10487-11	Sequence 11, Appl
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1076	75	1.9	809	1	US-08-487-203A-4	Sequence 4, Appli
1077	75	1.9	929	4	US-09-697-022-3	Sequence 3, Appli
1078	75	1.9	998	4	US-10-101-464A-931	Sequence 931, App
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1085	75	1.9	1059	4	US-09-905-125A-290	Sequence 290, App
1086	75	1.9	1059	4	US-09-902-775A-290	Sequence 290, App
1087	75	1.9	1059	4	US-09-906-700-290	Sequence 290, App
1088	75	1.9	1059	4	US-09-903-603A-290	Sequence 290, App
1089	75	1.9	1059	4	US-09-904-920A-290	Sequence 290, App
1090	75	1.9	1059	4	US-09-909-064-290	Sequence 290, App
1091	75	1.9	1059	4	US-09-905-381A-290	Sequence 290, App
1092	75	1.9	1059	4	US-09-906-618-290	Sequence 290, App
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1099	75	1.9	1119	4	US-09-906-700-294	Sequence 294, App
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1109	75	1.9	1457	2	US-08-991-258A-3	Sequence 3, Appli
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1116	75	1.9	1605	4	US-09-940-316B-33	Sequence 33, Appl
1117	75	1.9	1611	2	US-08-804-227C-5	Sequence 5, Appli
1118	75	1.9	2190	4	US-09-252-991A-25754	Sequence 25754, A
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1121	75	1.9	2324	4	US-09-902-540-9732	Sequence 9732, Ap
1122	75	1.9	2324	5	PCT-US95-09819-1	Sequence 1, Appli
1123	75	1.9	2327	6	5455158-1	Patent No. 5455158
1124	75	1.9	2327	6	5455158-1	Patent No. 5455158
1125	75	1.9	2446	2	US-08-551-356-2	Sequence 2, Appli
1126	75	1.9	2446	5	PCT-US93-12687-2	Sequence 2, Appli
1127	75	1.9	3491	2	US-07-642-734C-2	Sequence 2, Appli
1128	75	1.9	3491	3	US-08-439-009A-2	Sequence 2, Appli
1129	74.5	1.8	176	4	US-09-252-991A-21933	Sequence 21933, A
1130	74.5	1.8	217	4	US-09-391-606-7	Sequence 7, Appli
1131	74.5	1.8	268	4	US-09-248-796A-18252	Sequence 18252, A
1132	74.5	1.8	306	4	US-09-248-796A-18343	Sequence 18343, A
1133	74.5	1.8	316	3	US-09-308-375-3	Sequence 3, Appli
1134	74.5	1.8	316	4	US-09-932-183A-3	Sequence 3, Appli
1135	74.5	1.8	321	4	US-09-134-000C-4717	Sequence 4717, Ap
1136	74.5	1.8	343	3	US-08-978-741-17	Sequence 17, Appl
1137	74.5	1.8	343	3	US-09-333-729A-13	Sequence 13, Appl
1138	74.5	1.8	365	3	US-09-113-309-2	Sequence 2, Appli
1139	74.5	1.8	365	3	US-09-521-109-2	Sequence 2, Appli
1140	74.5	1.8	365	3	US-09-562-332-2	Sequence 2, Appli
1141	74.5	1.8	365	4	US-09-949-016-6436	Sequence 6436, Ap
1142	74.5	1.8	376	3	US-08-874-569B-20	Sequence 20, Appl
1143	74.5	1.8	376	4	US-09-955-518-20	Sequence 20, Appl
1144	74.5	1.8	390	4	US-09-252-991A-29855	Sequence 29855, A
1145	74.5	1.8	398	4	US-09-902-540-12305	Sequence 12305, A
1146	74.5	1.8	409	4	US-09-071-035-316	Sequence 316, App
1147	74.5	1.8	431	1	US-08-190-802A-37	Sequence 37, Appl
1148	74.5	1.8	431	3	US-08-477-346-37	Sequence 37, Appl
1149	74.5	1.8	431	3	US-08-473-089-37	Sequence 37, Appl
1150	74.5	1.8	431	4	US-08-487-072A-37	Sequence 37, Appl
1151	74.5	1.8	431	4	US-09-538-092-1267	Sequence 1267, Ap

1152	74.5	1.8	433	4	US-09-071-035-314	Sequence 314, App
1153	74.5	1.8	458	4	US-09-902-540-12784	Sequence 12784, A
1154	74.5	1.8	464	4	US-09-949-016-10463	Sequence 10463, A
1155	74.5	1.8	467	3	US-08-867-611-24	Sequence 24, Appl
1156	74.5	1.8	467	4	US-09-690-359-24	Sequence 24, Appl
1157	74.5	1.8	467	5	PCT-US92-06965A-29	Sequence 29, Appl
1158	74.5	1.8	489	4	US-09-902-540-16694	Sequence 16694, A
1159	74.5	1.8	519	4	US-09-949-016-7883	Sequence 7883, Ap
1160	74.5	1.8	525	3	US-08-888-949-16	Sequence 16, Appl
1161	74.5	1.8	525	3	US-08-888-950-16	Sequence 16, Appl
1162	74.5	1.8	525	3	US-09-262-758-16	Sequence 16, Appl
1163	74.5	1.8	525	4	US-09-885-876-16	Sequence 16, Appl
1164	74.5	1.8	525	4	US-09-885-901-16	Sequence 16, Appl
1165	74.5	1.8	525	4	US-09-731-393-16	Sequence 16, Appl
1166	74.5	1.8	527	1	US-08-805-814-10	Sequence 10, Appl
1167	74.5	1.8	527	1	US-08-484-815-10	Sequence 10, Appl
1168	74.5	1.8	527	3	US-08-888-949-10	Sequence 10, Appl
1169	74.5	1.8	527	3	US-08-888-950-10	Sequence 10, Appl
1170	74.5	1.8	527	3	US-09-262-758-10	Sequence 10, Appl
1171	74.5	1.8	527	4	US-09-885-876-10	Sequence 10, Appl
1172	74.5	1.8	527	4	US-09-885-901-10	Sequence 10, Appl
1173	74.5	1.8	527	4	US-09-489-039A-8627	Sequence 8627, Ap
1174	74.5	1.8	527	4	US-09-731-393-10	Sequence 10, Appl
1175	74.5	1.8	527	4	US-09-882-694B-13	Sequence 13, Appl
1176	74.5	1.8	527	5	PCT-US95-10284-10	Sequence 10, Appl
1177	74.5	1.8	537	1	US-08-472-028A-2	Sequence 2, Appli
1178	74.5	1.8	537	2	US-08-808-931-2	Sequence 2, Appli
1179	74.5	1.8	537	3	US-08-808-323-2	Sequence 2, Appli
1180	74.5	1.8	537	3	US-09-050-603A-2	Sequence 2, Appli
1181	74.5	1.8	537	3	US-09-102-420B-2	Sequence 2, Appli
1182	74.5	1.8	537	3	US-09-071-296-2	Sequence 2, Appli
1183	74.5	1.8	537	3	US-09-196-268-2	Sequence 2, Appli
1184	74.5	1.8	537	3	US-09-015-683-2	Sequence 2, Appli
1185	74.5	1.8	537	3	US-09-191-998-2	Sequence 2, Appli
1186	74.5	1.8	537	3	US-09-497-698-2	Sequence 2, Appli
1187	74.5	1.8	537	4	US-09-730-525-2	Sequence 2, Appli
1188	74.5	1.8	564	3	US-09-442-100-15	Sequence 15, Appl
1189	74.5	1.8	564	4	US-08-939-106-15	Sequence 15, Appl
1190	74.5	1.8	564	4	US-09-442-102-15	Sequence 15, Appl
1191	74.5	1.8	597	4	US-09-248-796A-14379	Sequence 14379, A
1192	74.5	1.8	608	4	US-09-369-247-68	Sequence 68, Appl
1193	74.5	1.8	639	4	US-09-902-540-14902	Sequence 14902, A
1194	74.5	1.8	659	4	US-09-562-737-13	Sequence 13, Appl
1195	74.5	1.8	685	4	US-09-949-016-8627	Sequence 8627, Ap
1196	74.5	1.8	701	4	US-09-710-279-710	Sequence 710, App
1197	74.5	1.8	703	3	US-09-134-001C-3015	Sequence 3015, Ap
1198	74.5	1.8	837	4	US-09-122-126B-2	Sequence 2, Appli
1199	74.5	1.8	837	4	US-09-634-286A-2	Sequence 2, Appli
1200	74.5	1.8	837	4	US-10-247-685-2	Sequence 2, Appli
1201	74.5	1.8	846	1	US-08-357-598-12	Sequence 12, Appl
1202	74.5	1.8	846	2	US-09-003-289-12	Sequence 12, Appl
1203	74.5	1.8	846	5	PCT-US95-16435-12	Sequence 12, Appl
1204	74.5	1.8	858	4	US-09-538-092-674	Sequence 674, App
1205	74.5	1.8	868	5	PCT-US95-08493-21	Sequence 21, Appl
1206	74.5	1.8	953	4	US-09-751-389-7	Sequence 7, Appli
1207	74.5	1.8	967	2	US-08-449-645A-30	Sequence 30, Appl
1208	74.5	1.8	967	2	US-08-702-367A-30	Sequence 30, Appl

1209	74.5	1.8	975	4	US-09-751-389-8	Sequence 8, Appli
1210	74.5	1.8	981	4	US-09-252-991A-18616	Sequence 18616, A
1211	74.5	1.8	1025	2	US-08-530-792D-23	Sequence 23, Appl
1212	74.5	1.8	1026	2	US-08-530-792D-22	Sequence 22, Appl
1213	74.5	1.8	1050	2	US-08-817-090B-4	Sequence 4, Appli
1214	74.5	1.8	1070	3	US-08-922-635-22	Sequence 22, Appl
1215	74.5	1.8	1089	4	US-09-949-016-10326	Sequence 10326, A
1216	74.5	1.8	1167	3	US-08-857-076-48	Sequence 48, Appl
1217	74.5	1.8	1271	4	US-09-540-236-3740	Sequence 3740, Ap
1218	74.5	1.8	1310	4	US-09-170-496D-290	Sequence 290, App
1219	74.5	1.8	1310	4	US-09-364-425B-55	Sequence 55, Appl
1220	74.5	1.8	1331	4	US-09-949-016-6861	Sequence 6861, Ap
1221	74.5	1.8	1387	4	US-09-902-540-11948	Sequence 11948, A
1222	74.5	1.8	1504	4	US-09-364-206-2	Sequence 2, Appli
1223	74.5	1.8	1578	4	US-09-410-551B-31	Sequence 31, Appl
1224	74.5	1.8	1578	4	US-09-940-316B-31	Sequence 31, Appl
1225	74.5	1.8	1607	4	US-09-902-540-16765	Sequence 16765, A
1226	74.5	1.8	1739	4	US-09-795-061-2	Sequence 2, Appli
1227	74.5	1.8	2183	3	US-08-746-111-5	Sequence 5, Appli
1228	74.5	1.8	2220	4	US-09-949-016-9730	Sequence 9730, Ap
1229	74.5	1.8	2308	1	US-08-015-973-1	Sequence 1, Appli
1230	74.5	1.8	2308	2	US-08-448-164-1	Sequence 1, Appli
1231	74.5	1.8	2308	3	US-08-081-929-2	Sequence 2, Appli
1232	74.5	1.8	2308	4	US-10-000-954-2	Sequence 2, Appli
1233	74.5	1.8	2314	4	US-09-816-703A-2	Sequence 2, Appli
1234	74.5	1.8	3340	4	US-09-252-991A-23568	Sequence 23568, A
1235	74.5	1.8	15281	2	US-08-471-119A-2	Sequence 2, Appli
1236	74	1.8	201	4	US-09-252-991A-28200	Sequence 28200, A
1237	74	1.8	228	4	US-09-634-238-329	Sequence 329, App
1238	74	1.8	258	4	US-09-579-845-9	Sequence 9, Appli
1239	74	1.8	276	3	US-09-094-964-1	Sequence 1, Appli
1240	74	1.8	276	3	US-09-094-964-2	Sequence 2, Appli
1241	74	1.8	343	3	US-09-363-189B-4	Sequence 4, Appli
1242	74	1.8	345	4	US-09-252-991A-27947	Sequence 27947, A
1243	74	1.8	409	2	US-09-031-485-15	Sequence 15, Appl
1244	74	1.8	409	2	US-08-847-429A-15	Sequence 15, Appl
1245	74	1.8	409	3	US-09-065-474-15	Sequence 15, Appl
1246	74	1.8	409	3	US-09-557-034-15	Sequence 15, Appl
1247	74	1.8	413	4	US-09-328-352-7815	Sequence 7815, Ap
1248	74	1.8	422	3	US-09-065-474-142	Sequence 142, App
1249	74	1.8	422	3	US-09-557-034-142	Sequence 142, App
1250	74	1.8	432	4	US-09-710-279-2942	Sequence 2942, Ap
1251	74	1.8	434	3	US-09-540-245A-19	Sequence 19, Appl
1252	74	1.8	445	4	US-09-252-991A-22912	Sequence 22912, A
1253	74	1.8	450	4	US-09-949-016-9225	Sequence 9225, Ap
1254	74	1.8	467	3	US-09-134-001C-5301	Sequence 5301, Ap
1255	74	1.8	495	4	US-09-734-237B-62	Sequence 62, Appl
1256	74	1.8	496	4	US-09-949-016-8278	Sequence 8278, Ap
1257	74	1.8	496	4	US-09-734-237B-64	Sequence 64, Appl
1258	74	1.8	512	3	US-08-426-509A-16	Sequence 16, Appl
1259	74	1.8	512	4	US-08-232-545-16	Sequence 16, Appl
1260	74	1.8	512	5	PCT-US95-05008-16	Sequence 16, Appl
1261	74	1.8	533	4	US-09-549-519-32	Sequence 32, Appl
1262	74	1.8	549	4	US-09-270-767-45421	Sequence 45421, A
1263	74	1.8	575	3	US-08-913-805A-2	Sequence 2, Appli
1264	74	1.8	575	3	US-09-442-629-2	Sequence 2, Appli
1265	74	1.8	583	2	US-08-432-016-2	Sequence 2, Appli

1266	74	1.8	583	2	US-08-684-594-2	Sequence 2, Appli
1267	74	1.8	613	4	US-09-170-496D-92	Sequence 92, Appl
1268	74	1.8	613	4	US-09-170-496D-212	Sequence 212, App
1269	74	1.8	639	4	US-09-782-906-4	Sequence 4, Appli
1270	74	1.8	652	4	US-09-252-991A-30872	Sequence 30872, A
1271	74	1.8	735	4	US-09-321-589-1	Sequence 1, Appli
1272	74	1.8	735	4	US-10-293-478-1	Sequence 1, Appli
1273	74	1.8	747	3	US-09-724-864-36	Sequence 36, Appl
1274	74	1.8	758	4	US-09-438-185A-926	Sequence 926, App
1275	74	1.8	769	3	US-08-434-000A-10	Sequence 10, Appl
1276	74	1.8	769	3	US-09-312-157-10	Sequence 10, Appl
1277	74	1.8	769	4	US-09-717-888-10	Sequence 10, Appl
1278	74	1.8	778	4	US-09-248-796A-15468	Sequence 15468, A
1279	74	1.8	850	4	US-09-949-016-11324	Sequence 11324, A
1280	74	1.8	985	5	PCT-US96-03916-6	Sequence 6, Appli
1281	74	1.8	985	5	PCT-US96-03916-66	Sequence 66, Appl
1282	74	1.8	1004	4	US-09-489-039A-9715	Sequence 9715, Ap
1283	74	1.8	1007	4	US-10-014-269-34	Sequence 34, Appl
1284	74	1.8	1013	4	US-10-014-269-3	Sequence 3, Appli
1285	74	1.8	1040	4	US-10-014-269-2	Sequence 2, Appli
1286	74	1.8	1043	4	US-09-949-016-9080	Sequence 9080, Ap
1287	74	1.8	1142	3	US-09-061-709-2	Sequence 2, Appli
1288	74	1.8	1142	4	US-09-899-651-2	Sequence 2, Appli
1289	74	1.8	1142	4	US-09-392-714-26	Sequence 26, Appl
1290	74	1.8	1142	4	US-09-270-437D-2	Sequence 2, Appli
1291	74	1.8	1269	4	US-09-902-540-15558	Sequence 15558, A
1292	74	1.8	1589	3	US-09-356-952-4	Sequence 4, Appli
1293	74	1.8	2325	3	US-08-417-089-6	Sequence 6, Appli
1294	74	1.8	2325	3	US-08-695-651-6	Sequence 6, Appli
1295	74	1.8	2325	3	US-08-930-285-6	Sequence 6, Appli
1296	74	1.8	2325	3	US-08-695-421-6	Sequence 6, Appli
1297	74	1.8	2325	4	US-08-697-826A-10	Sequence 10, Appl
1298	74	1.8	2873	1	US-08-466-033-15	Sequence 15, Appl
1299	74	1.8	2873	1	US-08-638-911A-2	Sequence 2, Appli
1300	74	1.8	2873	2	US-08-444-733-15	Sequence 15, Appl
1301	74	1.8	2873	2	US-08-464-134-15	Sequence 15, Appl
1302	74	1.8	2873	2	US-08-461-361-15	Sequence 15, Appl
1303	74	1.8	2873	2	US-08-485-910-15	Sequence 15, Appl
1304	74	1.8	2873	5	PCT-US95-06266-15	Sequence 15, Appl
1305	74	1.8	5032	4	US-09-538-092-979	Sequence 979, App
1306	74	1.8	5405	3	US-08-718-388-9	Sequence 9, Appli
1307	73.5	1.8	200	4	US-09-252-991A-22497	Sequence 22497, A
1308	73.5	1.8	208	4	US-09-270-767-43741	Sequence 43741, A
1309	73.5	1.8	254	4	US-09-134-000C-4199	Sequence 4199, Ap
1310	73.5	1.8	312	4	US-09-149-476-482	Sequence 482, App
1311	73.5	1.8	317	1	US-07-880-913-2	Sequence 2, Appli
1312	73.5	1.8	323	4	US-09-248-796A-16301	Sequence 16301, A
1313	73.5	1.8	346	4	US-09-949-016-7530	Sequence 7530, Ap
1314	73.5	1.8	368	3	US-08-991-677-6	Sequence 6, Appli
1315	73.5	1.8	403	4	US-09-328-352-5461	Sequence 5461, Ap
1316	73.5	1.8	463	4	US-09-252-991A-30002	Sequence 30002, A
1317	73.5	1.8	480	2	US-08-828-488-8	Sequence 8, Appli
1318	73.5	1.8	480	3	US-09-299-689A-8	Sequence 8, Appli
1319	73.5	1.8	480	4	US-09-702-705-336	Sequence 336, App
1320	73.5	1.8	480	4	US-09-736-457-336	Sequence 336, App
1321	73.5	1.8	480	4	US-09-614-124B-336	Sequence 336, App
1322	73.5	1.8	480	4	US-09-671-325-336	Sequence 336, App

1323	73.5	1.8	480	4	US-09-589-184-336	Sequence 336, App
1324	73.5	1.8	480	4	US-09-658-824-336	Sequence 336, App
1325	73.5	1.8	511	4	US-09-917-265A-67	Sequence 67, Appl
1326	73.5	1.8	515	4	US-09-252-991A-28687	Sequence 28687, A
1327	73.5	1.8	533	4	US-09-917-265A-62	Sequence 62, Appl
1328	73.5	1.8	538	4	US-09-489-039A-8363	Sequence 8363, Ap
1329	73.5	1.8	622	4	US-09-499-846-2	Sequence 2, Appli
1330	73.5	1.8	632	4	US-09-949-016-6976	Sequence 6976, Ap
1331	73.5	1.8	651	4	US-09-902-540-14740	Sequence 14740, A
1332	73.5	1.8	714	2	US-08-859-201-2	Sequence 2, Appli
1333	73.5	1.8	714	4	US-09-543-681A-6809	Sequence 6809, Ap
1334	73.5	1.8	714	4	US-09-402-214-2	Sequence 2, Appli
1335	73.5	1.8	732	3	US-08-914-999-8	Sequence 8, Appli
1336	73.5	1.8	740	4	US-09-248-796A-17732	Sequence 17732, A
1337	73.5	1.8	799	3	US-08-909-954-4	Sequence 4, Appli
1338	73.5	1.8	818	4	US-09-248-796A-18342	Sequence 18342, A
1339	73.5	1.8	820	1	US-07-921-807B-3	Sequence 3, Appli
1340	73.5	1.8	820	1	US-08-441-944A-3	Sequence 3, Appli
1341	73.5	1.8	820	3	US-08-439-992A-1	Sequence 1, Appli
1342	73.5	1.8	832	4	US-08-591-502B-62	Sequence 62, Appl
1343	73.5	1.8	862	4	US-09-751-687-9	Sequence 9, Appli
1344	73.5	1.8	862	4	US-09-751-687-12	Sequence 12, Appl
1345	73.5	1.8	879	1	US-08-554-612C-1	Sequence 1, Appli
1346	73.5	1.8	898	4	US-09-585-858-37	Sequence 37, Appl
1347	73.5	1.8	898	4	US-10-270-878-37	Sequence 37, Appl
1348	73.5	1.8	899	4	US-09-902-540-14878	Sequence 14878, A
1349	73.5	1.8	977	2	US-08-673-789-8	Sequence 8, Appli
1350	73.5	1.8	994	4	US-09-902-540-13822	Sequence 13822, A
1351	73.5	1.8	1040	4	US-10-014-269-4	Sequence 4, Appli
1352	73.5	1.8	1079	2	US-08-929-967-8	Sequence 8, Appli
1353	73.5	1.8	1122	4	US-09-711-164-451	Sequence 451, App
1354	73.5	1.8	1133	4	US-09-902-540-12243	Sequence 12243, A
1355	73.5	1.8	1239	2	US-08-231-193A-52	Sequence 52, Appl
1356	73.5	1.8	1239	2	US-08-486-273A-52	Sequence 52, Appl
1357	73.5	1.8	1239	3	US-08-480-474-52	Sequence 52, Appl
1358	73.5	1.8	1239	3	US-08-940-086A-52	Sequence 52, Appl
1359	73.5	1.8	1239	3	US-08-940-035A-52	Sequence 52, Appl
1360	73.5	1.8	1239	3	US-08-935-105A-52	Sequence 52, Appl
1361	73.5	1.8	1239	4	US-09-648-797-52	Sequence 52, Appl
1362	73.5	1.8	1239	4	US-09-386-123-52	Sequence 52, Appl
1363	73.5	1.8	1239	4	US-10-038-937-52	Sequence 52, Appl
1364	73.5	1.8	1244	2	US-08-231-193A-46	Sequence 46, Appl
1365	73.5	1.8	1244	2	US-08-486-273A-46	Sequence 46, Appl
1366	73.5	1.8	1244	3	US-08-480-474-46	Sequence 46, Appl
1367	73.5	1.8	1244	3	US-08-940-086A-46	Sequence 46, Appl
1368	73.5	1.8	1244	3	US-08-940-035A-46	Sequence 46, Appl
1369	73.5	1.8	1244	3	US-08-935-105A-46	Sequence 46, Appl
1370	73.5	1.8	1244	4	US-09-648-797-46	Sequence 46, Appl
1371	73.5	1.8	1244	4	US-09-386-123-46	Sequence 46, Appl
1372	73.5	1.8	1244	4	US-10-038-937-46	Sequence 46, Appl
1373	73.5	1.8	1280	4	US-09-377-285B-18	Sequence 18, Appl
1374	73.5	1.8	1336	2	US-08-551-356-6	Sequence 6, Appli
1375	73.5	1.8	1336	5	PCT-US93-12687-6	Sequence 6, Appli
1376	73.5	1.8	1737	4	US-09-309-572-13	Sequence 13, Appl
1377	73.5	1.8	1737	4	US-09-718-096-13	Sequence 13, Appl
1378	73.5	1.8	2321	4	US-09-230-652-2	Sequence 2, Appli
1379	73.5	1.8	2780	4	US-10-220-587-2	Sequence 2, Appli

1380	73.5	1.8	2907	4	US-09-698-295-1	Sequence 1, Appli
1381	73	1.8	161	4	US-09-252-991A-27444	Sequence 27444, A
1382	73	1.8	217	4	US-09-107-433-4763	Sequence 4763, Ap
1383	73	1.8	322	3	US-09-199-637A-49	Sequence 49, Appl
1384	73	1.8	336	4	US-09-252-991A-17738	Sequence 17738, A
1385	73	1.8	361	3	US-08-874-569B-21	Sequence 21, Appl
1386	73	1.8	361	4	US-09-955-518-21	Sequence 21, Appl
1387	73	1.8	416	2	US-09-000-846-2	Sequence 2, Appli
1388	73	1.8	440	2	US-08-808-931-24	Sequence 24, Appl
1389	73	1.8	440	3	US-08-808-323-24	Sequence 24, Appl
1390	73	1.8	440	3	US-09-050-603A-24	Sequence 24, Appl
1391	73	1.8	440	3	US-09-102-420B-24	Sequence 24, Appl
1392	73	1.8	440	3	US-09-497-698-24	Sequence 24, Appl
1393	73	1.8	440	4	US-09-730-525-24	Sequence 24, Appl
1394	73	1.8	447	4	US-09-902-540-10788	Sequence 10788, A
1395	73	1.8	449	2	US-08-839-008-2	Sequence 2, Appli
1396	73	1.8	458	4	US-09-949-016-7238	Sequence 7238, Ap
1397	73	1.8	466	4	US-09-270-767-60926	Sequence 60926, A
1398	73	1.8	472	3	US-09-088-425-1	Sequence 1, Appli
1399	73	1.8	472	4	US-09-639-378A-1	Sequence 1, Appli
1400	73	1.8	544	3	US-09-087-134-14	Sequence 14, Appl
1401	73	1.8	544	4	US-09-489-039A-13133	Sequence 13133, A
1402	73	1.8	555	4	US-09-252-991A-30276	Sequence 30276, A
1403	73	1.8	603	4	US-09-252-991A-17711	Sequence 17711, A
1404	73	1.8	609	3	US-09-232-200-69	Sequence 69, Appl
1405	73	1.8	609	3	US-09-232-197-69	Sequence 69, Appl
1406	73	1.8	609	3	US-09-232-201-69	Sequence 69, Appl
1407	73	1.8	609	4	US-09-232-195-69	Sequence 69, Appl
1408	73	1.8	613	3	US-09-232-191-7	Sequence 7, Appli
1409	73	1.8	613	3	US-09-232-200-7	Sequence 7, Appli
1410	73	1.8	613	3	US-09-232-200-94	Sequence 94, Appl
1411	73	1.8	613	3	US-09-232-197-7	Sequence 7, Appli
1412	73	1.8	613	3	US-09-232-197-94	Sequence 94, Appl
1413	73	1.8	613	3	US-09-232-201-7	Sequence 7, Appli
1414	73	1.8	613	3	US-09-232-201-94	Sequence 94, Appl
1415	73	1.8	613	4	US-09-232-195-7	Sequence 7, Appli
1416	73	1.8	613	4	US-09-232-195-94	Sequence 94, Appl
1417	73	1.8	693	4	US-09-538-092-534	Sequence 534, App
1418	73	1.8	701	4	US-09-252-991A-32462	Sequence 32462, A
1419	73	1.8	709	4	US-09-949-016-6809	Sequence 6809, Ap
1420	73	1.8	719	4	US-09-902-540-11526	Sequence 11526, A
1421	73	1.8	728	4	US-09-949-016-7213	Sequence 7213, Ap
1422	73	1.8	750	4	US-09-949-016-7201	Sequence 7201, Ap
1423	73	1.8	750	4	US-09-949-016-7202	Sequence 7202, Ap
1424	73	1.8	822	4	US-08-684-932A-38	Sequence 38, Appl
1425	73	1.8	822	4	US-09-618-304B-2	Sequence 2, Appli
1426	73	1.8	832	4	US-08-591-502B-64	Sequence 64, Appl
1427	73	1.8	845	4	US-08-591-502B-58	Sequence 58, Appl
1428	73	1.8	845	6	5196194-17	Patent No. 5196194
1429	73	1.8	845	6	5196194-17	Patent No. 5196194
1430	73	1.8	849	4	US-09-949-016-8846	Sequence 8846, Ap
1431	73	1.8	849	4	US-09-949-016-8847	Sequence 8847, Ap
1432	73	1.8	853	4	US-09-949-016-8275	Sequence 8275, Ap
1433	73	1.8	853	4	US-09-949-016-8276	Sequence 8276, Ap
1434	73	1.8	863	4	US-09-489-039A-10179	Sequence 10179, A
1435	73	1.8	892	4	US-09-248-796A-19224	Sequence 19224, A
1436	73	1.8	964	4	US-09-902-540-14068	Sequence 14068, A

1437	73	1.8	974	4	US-09-856-930-2	Sequence 2, Appli
1438	73	1.8	984	2	US-08-673-789-9	Sequence 9, Appli
1439	73	1.8	1149	3	US-08-560-005-5	Sequence 5, Appli
1440	73	1.8	1149	3	US-09-418-540-5	Sequence 5, Appli
1441	73	1.8	1149	4	US-09-969-528-5	Sequence 5, Appli
1442	73	1.8	1876	4	US-09-418-710-71	Sequence 71, Appl
1443	73	1.8	1876	4	US-09-839-479-70	Sequence 70, Appl
1444	73	1.8	1909	4	US-09-590-968B-2	Sequence 2, Appli
1445	73	1.8	1911	1	US-08-348-006B-5	Sequence 5, Appli
1446	73	1.8	1911	2	US-08-800-825A-5	Sequence 5, Appli
1447	73	1.8	1911	3	US-09-158-657-5	Sequence 5, Appli
1448	73	1.8	1911	5	PCT-US94-10166-5	Sequence 5, Appli
1449	72.5	1.8	242	4	US-09-345-236B-3	Sequence 3, Appli
1450	72.5	1.8	356	3	US-09-500-569-6	Sequence 6, Appli
1451	72.5	1.8	356	4	US-09-971-823B-6	Sequence 6, Appli
1452	72.5	1.8	360	4	US-09-252-991A-23898	Sequence 23898, A
1453	72.5	1.8	395	4	US-09-602-777A-208	Sequence 208, App
1454	72.5	1.8	395	4	US-09-602-777A-210	Sequence 210, App
1455	72.5	1.8	402	1	US-08-314-309A-6	Sequence 6, Appli
1456	72.5	1.8	410	4	US-09-949-016-7021	Sequence 7021, Ap
1457	72.5	1.8	414	4	US-09-540-236-2868	Sequence 2868, Ap
1458	72.5	1.8	421	4	US-09-902-540-13318	Sequence 13318, A
1459	72.5	1.8	423	3	US-08-702-665A-5	Sequence 5, Appli
1460	72.5	1.8	437	4	US-09-248-796A-19198	Sequence 19198, A
1461	72.5	1.8	441	1	US-08-314-309A-4	Sequence 4, Appli
1462	72.5	1.8	453	4	US-09-252-991A-25795	Sequence 25795, A
1463	72.5	1.8	485	3	US-09-320-878-10	Sequence 10, Appl
1464	72.5	1.8	485	3	US-09-105-537-10	Sequence 10, Appl
1465	72.5	1.8	485	4	US-09-141-908-23	Sequence 23, Appl
1466	72.5	1.8	485	4	US-09-657-440-10	Sequence 10, Appl
1467	72.5	1.8	521	4	US-09-270-767-43965	Sequence 43965, A
1468	72.5	1.8	531	4	US-09-949-016-7044	Sequence 7044, Ap
1469	72.5	1.8	533	2	US-08-225-488-2	Sequence 2, Appli
1470	72.5	1.8	540	2	US-08-884-072-3	Sequence 3, Appli
1471	72.5	1.8	540	3	US-09-212-168-3	Sequence 3, Appli
1472	72.5	1.8	540	4	US-09-513-057C-33	Sequence 33, Appl
1473	72.5	1.8	540	4	US-09-854-549A-2	Sequence 2, Appli
1474	72.5	1.8	540	4	US-09-660-107-13	Sequence 13, Appl
1475	72.5	1.8	540	4	US-09-746-801A-33	Sequence 33, Appl
1476	72.5	1.8	566	1	US-07-955-905A-2	Sequence 2, Appli
1477	72.5	1.8	566	1	US-07-955-905A-22	Sequence 22, Appl
1478	72.5	1.8	568	4	US-09-949-016-7970	Sequence 7970, Ap
1479	72.5	1.8	582	1	US-08-261-086-2	Sequence 2, Appli
1480	72.5	1.8	582	1	US-08-261-086-4	Sequence 4, Appli
1481	72.5	1.8	582	1	US-08-261-086-6	Sequence 6, Appli
1482	72.5	1.8	584	4	US-09-842-307-2	Sequence 2, Appli
1483	72.5	1.8	594	4	US-09-107-532A-6929	Sequence 6929, Ap
1484	72.5	1.8	617	4	US-09-614-912-138	Sequence 138, App
1485	72.5	1.8	637	4	US-09-902-540-10450	Sequence 10450, A
1486	72.5	1.8	651	4	US-09-270-767-44877	Sequence 44877, A
1487	72.5	1.8	677	2	US-08-522-269B-3	Sequence 3, Appli
1488	72.5	1.8	677	3	US-09-294-923-3	Sequence 3, Appli
1489	72.5	1.8	722	3	US-09-433-043B-125	Sequence 125, App
1490	72.5	1.8	736	3	US-09-102-528-29	Sequence 29, Appl
1491	72.5	1.8	737	4	US-09-955-732A-13	Sequence 13, Appl
1492	72.5	1.8	755	4	US-09-134-000C-6691	Sequence 6691, Ap
1493	72.5	1.8	837	4	US-09-489-039A-9385	Sequence 9385, Ap

1494	72.5	1.8	871	3	US-09-245-041-19	Sequence 19, Appl
1495	72.5	1.8	871	4	US-09-358-055B-19	Sequence 19, Appl
1496	72.5	1.8	871	4	US-09-893-238-19	Sequence 19, Appl
1497	72.5	1.8	974	4	US-10-101-464A-921	Sequence 921, App
1498	72.5	1.8	986	2	US-08-673-789-3	Sequence 3, Appli
1499	72.5	1.8	1012	1	US-08-219-262B-8	Sequence 8, Appli
1500	72.5	1.8	1012	3	US-09-031-655-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-578-063-19

; Sequence 19, Application US/09578063

; Patent No. 6764677

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A

; APPLICANT: Barnes, Thomas M

; APPLICANT: Fraser, Christopher C

; APPLICANT: Sharp, John D

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,

; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES

; FILE REFERENCE: 210147.0023/6U1

; CURRENT APPLICATION NUMBER: US/09/578,063

; CURRENT FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/333,159

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 79

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 761

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-578-063-19

Query Match 100.0%; Score 4031; DB 4; Length 761;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG	60
Db	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKS	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKS	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAaipst	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAaipst	240
Qy	241	QVYFFFEETASEDFFERLHtsrvarvckndvggekllqkkwttflkaqlLCTQPGQLP	300

Db	241		QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301		FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301		FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361		TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Db	361		TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421		ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421		ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481		VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481		VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541		GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541		GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601		ASSTVYNGSLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601		ASSTVYNGSLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661		VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCE	720
Db	661		VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCE	720
Qy	721		TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721		TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 2

US-09-578-063-21

; Sequence 21, Application US/09578063

; Patent No. 6764677

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A

; APPLICANT: Barnes, Thomas M

; APPLICANT: Fraser, Christopher C

; APPLICANT: Sharp, John D

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,

; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES

; FILE REFERENCE: 210147.0023/6U1

; CURRENT APPLICATION NUMBER: US/09/578,063

; CURRENT FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/333,159

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 79

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 730

; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-578-063-21

Query Match 96.1%; Score 3875; DB 4; Length 730;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 730; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GGGGQGMPRVRYAGDERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQD 60

Qy     92 PGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPAC 151
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Db     61 PGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPAC 120

Qy    152 TFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRT 211
          |||
Db    121 TFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRT 180

Qy    212 LGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFEETASEFDFFERLHTSRVARVCKN 271
          |||
Db    181 LGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFEETASEFDFFERLHTSRVARVCKN 240

Qy    272 DVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVG 331
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Db    241 DVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVG 300

Qy    332 GTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTF 391
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Db    301 GTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTF 360

Qy    392 MKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVVSGD 451
          |||
Db    361 MKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVVSGD 420

Qy    452 SSAHLVEEIQLFPDPEPVRNLQLAPTQGA VFVGFSGGVWRVPRANCSVYESCVDCVLARD 511
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Db    421 SSAHLVEEIQLFPDPEPVRNLQLAPTQGA VFVGFSGGVWRVPRANCSVYESCVDCVLARD 480

Qy    512 PHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAV 571
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Db    481 PHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAV 540

Qy    572 PNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENG F 631
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Db    541 PNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENG F 600

Qy    632 SYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLF 691
          |||
Db    601 SYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLF 660

Qy    692 ALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDA 751
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Db    661 ALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDA 720

Qy    752 DNNCLGTEVA 761
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RESULT 3

US-09-578-063-22

; Sequence 22, Application US/09578063
 ; Patent No. 6764677
 ; GENERAL INFORMATION:
 ; APPLICANT: McCarthy, Sean A
 ; APPLICANT: Barnes, Thomas M
 ; APPLICANT: Fraser, Christopher C
 ; APPLICANT: Sharp, John D
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
 ; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
 ; FILE REFERENCE: 210147.0023/6U1
 ; CURRENT APPLICATION NUMBER: US/09/578,063
 ; CURRENT FILING DATE: 2000-05-24
 ; PRIOR APPLICATION NUMBER: US 09/333,159
 ; PRIOR FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 652
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-578-063-22

Query Match 86.5%; Score 3486; DB 4; Length 652;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	92	PGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPAC	151
Db	61	PGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPAC	120
Qy	152	TFIELQDSYLLPISEDKVMGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRT	211
Db	121	TFIELQDSYLLPISEDKVMGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRT	180
Qy	212	LGSQPVLKTDNFLRWLHHDAFVAaipSTQVVYFFFEETASEFDFFERLHTSRVARVCKN	271
Db	181	LGSQPVLKTDNFLRWLHHDAFVAaipSTQVVYFFFEETASEFDFFERLHTSRVARVCKN	240
Qy	272	DVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVG	331
Db	241	DVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVG	300
Qy	332	GTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTF	391
Db	301	GTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTF	360
Qy	392	MKDHFLLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTTTGSLHKAVVSGD	451

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Db      361 MKDHFILMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVVSGD 420
Qy      452 SSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVYESCVDCVLARD 511
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Db      421 SSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVYESCVDCVLARD 480
Qy      512 PHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAV 571
        |||
Db      481 PHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAV 540
Qy      572 PNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENG 631
        |||
Db      541 PNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENG 600
Qy      632 SYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPH 683
        |||
Db      601 SYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPH 652

```

RESULT 4

US-09-578-063-70

; Sequence 70, Application US/09578063

; Patent No. 6764677

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A

; APPLICANT: Barnes, Thomas M

; APPLICANT: Fraser, Christopher C

; APPLICANT: Sharp, John D

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,

; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES

; FILE REFERENCE: 210147.0023/6U1

; CURRENT APPLICATION NUMBER: US/09/578,063

; CURRENT FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/333,159

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 79

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 70

; LENGTH: 760

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-578-063-70

Query Match 81.4%; Score 3280.5; DB 4; Length 760;

Best Local Similarity 82.3%; Pred. No. 0;

Matches 628; Conservative 46; Mismatches 84; Indels 5; Gaps 3;

```

Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPT--TTAGGGGQGPMPRVRYAGDERRALSFFHQ 58
        |||:| | | | | :| || | | | :| | | | | | | | | | | | | | | | |
Db      1 MALPSLGQDSWSLLRVFFQQL--FLLPSLPPASGTGGQGPMPRVKYHAGDGHRLSFFQQ 58
Qy      59 KGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKK 118
        |||:| | | | | | | | | | | | | | | :|||:| | :| | | | | | | | | | |
Db      59 KGLRDFDTLLLSDDGNTLYVGARETVLALNIQNPGIPRLKNMIWPASERKKTECAFKKK 118
Qy      119 SNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPF 178
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Db 119 SNETQCFNFIRVLVSYNATHLYACGTFAFSPACTFIELQDSLLLPIIDKVMGKGQSPL 178

Qy 179 DPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIP 238
 |||||

Db 179 TLFTSTQAVLVDGMLYSGTMNFLGSEPILMRTLGSHPVLKTDIFLRWLHADASFVAAIP 238

Qy 239 STQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ 298
 |||||

Db 239 STQVVYFFFEETASEFDFFELYISRVAQVCKNDVGGEKLLQKKWTTFLKAQLLCAQPGQ 298

Qy 299 LPFNVIIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELN 358
 |||||

Db 299 LPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELN 358

Qy 359 KETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMLMDEQVVGTPLLVKSGVEYTRL 418
 |||||

Db 359 KETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFMLMDEHVVGTPLLVKSGVEYTRL 418

Qy 419 AVETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQ 478
 |||||

Db 419 AVESARGLDGSSHVMYLGTTSTGPLHKAVVPQDSSAYLVEEIQLSPDPEPVRNLQLAPAQ 478

Qy 479 GAVFVGFGSGGVWRVPRANC SVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDM 538
 |||||

Db 479 GAVFAGFGSGGIWRVPRANC SVYESCVDCVLARDPHCAWDPE SRLCSLLSG-STKPWKQDM 537

Qy 539 ERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAV 598
 |||||

Db 538 ERGNPEWVCTRGP MARSRRQSPQLIKEVLTVPNSILELRCPHLSALASYHWSHGRAKI 597

Qy 599 PEASSTVYNGSLLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPR 658
 |||||

Db 598 SEASATVYNGSLLLLPQDGVGGLYQCWATENGYSYPVVSYWVDSQDQPLALDPELAGVPR 657

Qy 659 EHVKVPLTRVSGGAALAAQQSYWPHFVTVTVL FALVLSGALIILVASPLRALRARGKVQG 718
 |||||

Db 658 ERVQVPLTRVGGGASMAAQRSYWPHEFLIVTVLLAIVLLGVLTLLLASPLGALRARGKVQG 717

Qy 719 CETLRPGEKAPLSREQHLQSPKECRTSASD V DADNNCLGTEVA 761
 |||||

Db 718 CGMLPPREKAPLSRDQHLQPSKDHRTSASD V DADNNHLGAEVA 760

RESULT 5

US-09-578-063-76

; Sequence 76, Application US/09578063

; Patent No. 6764677

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A

; APPLICANT: Barnes, Thomas M

; APPLICANT: Fraser, Christopher C

; APPLICANT: Sharp, John D

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,

; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES

; FILE REFERENCE: 210147.0023/6U1

; CURRENT APPLICATION NUMBER: US/09/578,063

; CURRENT FILING DATE: 2000-05-24

```
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 760
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-578-063-76
```

Query Match 81.4%; Score 3280.5; DB 4; Length 760;
Best Local Similarity 82.3%; Pred. No. 0;
Matches 628; Conservative 46; Mismatches 84; Indels 5; Gaps 3;

Qy	1	MALPALGLDPWSLLGLFLFQLQLLLPT--TTAGGGGQGPMPrVRYAGDERRALSFFHQ	58
Db	1	MALPSLGGQDSWSLLRVFFFQL--FLLPSLPPASGTGGQGPMPrVKYHAGDGHRLSFFQQ	58
Qy	59	KGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKK	118
Db	59	KGLRDFDTLLLSDDGNTLYVGARETVLALNIQNPGIPRLKNMIPWPASERKKTECAFKKK	118
Qy	119	SNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPF	178
Db	119	SNETQCFNFIRVLVSYNATHLYACGTFAFSPACTFIELQDSLILIDKVMGKGQSPL	178
Qy	179	DPAKHHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIP	238
Db	179	TLFTSTQAVLVDGMLYSGTMNFLGSEPILMRTLGSHPVLKTDIFLRWLHADASFVAAIP	238
Qy	239	STQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ	298
Db	239	STQVVYFFFEETASEFDFFEEELYISRAVQVCKNDVGGEKLLQKKWTTFLKAQLLCAQPGQ	298
Qy	299	LPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELN	358
Db	299	LPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLTDIERVFKGKYKELN	358
Qy	359	KETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRL	418
Db	359	KETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFMLDEHVVGTPLLVKSGVEYTRL	418
Qy	419	AVETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQ	478
Db	419	AVESARGLDGSSHVMYLGTTSTGPLHKAVVPQDSSAYLVEEIQLSPDSEPVRNLQLAPAQ	478
Qy	479	GAVFVGFGSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDM	538
Db	479	GAVFAGFGSGGIWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCLLSG-STKPWKQDM	537
Qy	539	ERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAV	598
Db	538	ERGNPEWVCTRGPMARSPRRQSPPLIKEVLTVPNSILELRCPHLSALASYHWSHGRAKI	597
Qy	599	PEASSTVYNGSLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPR	658
Db	598	SEASATVYNGSLLLLPQDGVGGGLYQC VATENGYSYPVVSYWVDSQDQPLALDPELAGVPR	657

Db	297	GTTEGSAICVFTMNDVQKAFDGLYKKVNRETQQWYTETHQVPTPRPGACITNSARERKIN	356
Qy	385	-----SDKALTFMKDHFLLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHS-HLVMYLGT	438
Db	357	SSLQLPDRVLNFKDHFLLMDGQVRSRLLLQPRARYQRVAVHRVPGL--HSTYDVLFLGT	414
Qy	439	TTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAFFVGFSGGVWRVPRANCS	498
Db	415	GDGRLHKAVTL-SSRVHIIIEELQIFPQGGPVQNLLDSHGGLLYASSHSGVVQVPVANCS	473
Qy	499	VYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNS--WKQDMERGNPEWACASGPMSRSL	556
Db	474	LYPTCGDCLLARDPHYCAWTGSACRLASLYQPDLASRPWTQDIEGASVKELCKNSSYKARF	533
Qy	557	RPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAPVEASS--TVYNGSLLLI-	613
Db	534	LVPGKP--CKQVQIQPNTVNTLACPLLSNLATRLWVHNGAPVNASASCRVLPDGLLLVG	591
Qy	614	VQDGVGGGLYQCWATENG	630
Db	592	SQQGL-GVFQCSIEEG	607

RESULT 7

US-08-556-422A-2

```
; Sequence 2, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-08-556-422A-2

```
Query Match          25.9%; Score 1044; DB 4; Length 862;
Best Local Similarity 35.2%; Pred. No. 5.3e-95;
Matches 271; Conservative 115; Mismatches 263; Indels 120; Gaps 27;
```

Qy	38	PMPRVRYAGDERRALSF--FHQKGLQDFDTLLSGDGNTLYVGAREAILALDIQDPGVP	95
Db	26	PIPRITW-----EHREVHLVQFHEPDIYNYSALLLSEDKDTLYIGAREAVFAVNALN--IS	79
Qy	96	RLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIE	155
Db	80	EKQHEVYWKVSEDKKAKCAEKGKSKQTECLNYIRVLQPLSATSPLYVCGTNAFQACDHLN	139

; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 865
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-33

Query Match 23.8%; Score 961; DB 4; Length 865;
Best Local Similarity 33.8%; Pred. No. 1.1e-86;
Matches 267; Conservative 105; Mismatches 269; Indels 150; Gaps 29;

```
Qy      57 HQKG-LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPR LKNMIPWPASDRKKSECAF 115
      | | | | : : | | | | | | | | : : | | | | | | : : |
Db      48 HFKGQAQNYSTLLLEEASARLLVGARGALFSLSANDIGDGAHKE-IHWEASPEMQSKCHQ 106

Qy     116 KKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQ 175
      | | : : | : | | : | | | | | | | | | : : : | | : | | :
Db     107 KGKNNQTECFNHVRFLQRLNSTHLYACGTHAFQPLCAAID-AEAFTLPTSFE---EGKEK 162

Qy     176 SPFDPAHKHTAVLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHHDASFV- 234
      | : | | | | : : : | | | : | | | : | : : : | | : | | |
Db     163 CPYDPARGFTGLIIDGGLYTATRYEF-RSIPDIRRSRPHSLRTEETPMHWL-NDAEFVF 220

Qy     235 -----AAIPSTQVVYFFFEETASE-----FDFFERLH-TSRVARVCKNDVGGEKLL 279
      : | : | | : | | | | | | | | : | | | | | | | : | : | : |
Db     221 SVLVRESKASAVGDDDKVYFFTERATEEGSGSFTQSRSSHRVARVARVCKGDLGGKKIL 280

Qy     280 QKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFT--SQWQVGGTRSSA 337
      | | | | : | | | : | | : : | | : : | | | | : | : : |
Db     281 QKKWTSFLKARLICHIP---LYETLRGVCSLDAETSSRTHFYAAFTLSTQWKT--LEASA 335

Qy     338 VCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDK---- 387
      : | : | : | : | | | | : | | | | | | | | | | | : | :
Db     336 ICRYDLAEIQAVFAGPYMEYQDGSRRWGRYEGGVPEPRPGSCITDSLRSQGYNSSQDLPS 395

Qy     388 -ALTFMKDHF LMD EQVV---GTPLL VKSGVEYTRLAVETAQGLDGSHSLV MYLGTTT GSL 443
      | | : | | | | | | | | | | : | | | | | | | : : : | | | :
Db     396 LVLDFVKLHPLMARPVVPTGRGPLLLKRNIRYTHLTGTPVTTT PAGPTYDLLFLGTADGWI 455

Qy     444 HKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVYESC 503
      | | | | | | | : : | | : : | | : : | : : | | : : | | |
Db     456 HKAVVLG-SGMHIIETQVFRESQSVENLVISLLQHSLYVGAPSGVIQLPLSSCSRYRSC 514

Qy     504 VDCVLARDPHCAWDPE SRTCCLLSA-PNLNSWKQDMERGNPEWACASGPM SRSRLRPQSRP 562
      | | : | | | : | | : | : | | : | | : | | | | | | |
Db     515 YDCILARDPYCGWDPGTHACAAATTIANRTALIQDIERNR---GCES---SRDTGP---P 566

Qy     563 QIIKEVLAVPNSILELPCPHLSALASYYSW SHGPAAVPEASSTVYNGSLLLIVQDGVGGL- 621
      : | : : | | | | | | | : | | : | | | |
```

```

Db      567 PPLKTRSVLRGDDVLLPCDQPSNLRALW-----LLNGSMGL--SDGQGGYR 611
Qy      622 -----YQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKV 663
          | |:| ||| : || : : | | | : |
Db      612 VGVDGLLVTDAPQPEHSGNYGCYAEENGLRTLASYSLTVRPATPAPAPKAPATP----- 665
Qy      664 PLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPL----- 707
          || || | : : |: | | ::|| |
Db      666 -----GAQLAPD-----VRLLYVLAIAALGGLCLILASSLLYVACLREGRRRGRRRK 711
Qy      708 ----RALRARGKVQCET-----LRPGEKAPLS-----REQHLQSPKECRTS 745
          || || | :| : | :| | | : | | | |
Db      712 YSLGRASRAGGSAVQLQTVSGRALQVHMGSMSPPSAWPCVLDGPETRVLCQPPKPCVHS 771

Qy      746 ASDVDADNNCL 756
          : :: ||
Db      772 HAHME---ECL 779

```

RESULT 9

US-09-854-845-29

```

; Sequence 29, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 838
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-29

```

```

Query Match          23.8%; Score 958; DB 4; Length 838;.
Best Local Similarity 34.7%; Pred. No. 2.1e-86;
Matches 259; Conservative 101; Mismatches 255; Indels 132; Gaps 27;

```

```

Qy      57 HQKG-LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLLKNMIPWPASDRKKSECAF 115
          | || |:: |||| | |||| |: :| | | | | | | | :|:|
Db      48 HFKGQAQNYSTLLLEEASARLLVGARGALFSLSANDIGDAHKE-IHWEASPEMQSKCHQ 106

Qy      116 KKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQ 175
          | |:|:|:|||| :| | | |||| ||| || | | | : : : || | : ||| :
Db      107 KGKNNQTECFNHVRFLQRLNSTHLYACGTHAFQPLCAAID-AEAFTLPTSFE---EGKEK 162

```



```
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 870
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-31
```

```
Query Match          23.7%; Score 954.5; DB 4; Length 870;
Best Local Similarity 33.5%; Pred. No. 5.1e-86;
Matches 267; Conservative 105; Mismatches 269; Indels 155; Gaps 29;
```

```
Qy      57 HQKG-LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRCLKNMIPWPASDRKKSECAF 115
      | | | | : | | | | | | | | | | | | | | | | : | |
Db      48 HFKGQAQNYSTLLLEEASARLLVGARGALFSLSANDIGDGAHKE-IHWEASPEMQSKCHQ 106

Qy     116 KKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQ 175
      | | : | : | : | | | | | | | | | | | | | | : : : | | : | | :
Db     107 KGKNNQTECFNHVRFLQRLNSTHLYACGTHAFQPLCAAID-AEAFTLPTSFE---EGKEK 162

Qy     176 SPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHHDASFV- 234
      | : | | | | : : : | | | | | | | | : : : : : | | : | | | |
Db     163 CPYDPARGFTGLIIDGGLYTATRYEF-RSIPDIRRSRPHSLRTEETPMHWL-NDAEFVF 220

Qy     235 -----AAIPSTQVVYFFFEETASE-----FDFFERLH-TSRVARVCKNDVGGEKLL 279
      : | : | | : | | | | | | | | | | | | | | | | | : | : | : |
Db     221 SVLVRESKASAVGDDDKVYFFTERATEEGSGSFTQSRSSHRVARVARVCKGDLGGKKIL 280

Qy     280 QKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFT--SQWQVGGTRSSA 337
      | | | | : | | | : | | : : | | | | | | | | : | : : | |
Db     281 QKKWTSFLKARLICHIP---LYETLRGVCSLDAETSSRTHFYAAFTLSTQWKT--LEASA 335

Qy     338 VCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDK---- 387
      : | : | : | : | | | | | : | | | | | | | | | | | | : | :
Db     336 ICRYDLAEIQAVFAGPYMEYQDGSRRWGRYEGGVPEPRPGSCITDSLRSQGYNSSQDLPS 395

Qy     388 -ALTFMKDHFMLMDEQVV---GTPLLKSGVEYTRLAVETAQGLDGSHLVMYLGTTTGSL 443
      | | : | | | | | | | | | | | | | | | | | : : : : | | :
Db     396 LVLDFVKLHPLMARPVVPTGRPLLLKRNIRYTHLTGTPVTTTPAGPTYDLLFLGTADGWI 455

Qy     444 HKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVYESC 503
      | | | | | | | : | | | : : | | : : | : : | | : | : | | | |
Db     456 HKAVVLG-SGMHIIETQVFRESQSVENLVISLLQHSLYVGAPSGVIQLPLSSCSRYRSC 514

Qy     504 VDCVLARDPHCAWDPESTRCCLL-----SAPNLNSWKQDMERGNPEWACASGPMSRSLR 557
      | | : | | | | : | | | : : | | : | | | | | | | | | |
Db     515 YDCILARDPYCGWDPGTHACAAATTIANRSQGSRTALIQDIERGNR--GCES---SRDTG 569

Qy     558 PQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDG 617
      | | | : | : : | | | | | | | | | | | | | | : | | : | |
Db     570 P---PPPLKTRSVLRGDDVLLPCDQPSNLARALW-----LLNGSMGL--SDG 611
```

Qy 618 VGGL-----YQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPR 658
 || | : | || : | : | | : |
 Db 612 QGGYRVGVDGLLVTDQAQPEHSGNYGCGYAEENGLRLLASYSLTVRPATPAPAPKAPATP- 670
 Qy 659 EHVKVLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPL----- 707
 || || | : : | : | | : : || |
 Db 671 -----GAQLAPD-----VRLLYVLAIAALGGLCLILASSLLYVACLREGRR 711
 Qy 708 -----RALRARGKVQGCET-----LRPGEKAPLS-----REQHLQSPK 740
 || || | : | : | : | : | ||
 Db 712 GRRRKYSILGRASRAGGSAVQLQTVSGRALQVHMGSMSPPSAWPCVLDGPETROVLCQPPK 771
 Qy 741 ECRTSASDVDADNNCL 756
 | | : : ||
 Db 772 PCVHSHAHME---ECL 784

RESULT 11

US-09-854-845-27

; Sequence 27, Application US/09854845

; Patent No. 6750054

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Wang, Xiaoming

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6750054e1 Human Semaphorin Homologs and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0177-USA

; CURRENT APPLICATION NUMBER: US/09/854,845

; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: US 60/205,274

; PRIOR FILING DATE: 2000-05-18

; PRIOR APPLICATION NUMBER: US 60/208,893

; PRIOR FILING DATE: 2000-06-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 27

; LENGTH: 843

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-854-845-27

Query Match 23.6%; Score 951.5; DB 4; Length 843;

Best Local Similarity 34.4%; Pred. No. 9.6e-86;

Matches 259; Conservative 101; Mismatches 255; Indels 137; Gaps 27;

Qy 57 HQKG-LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLLKNMIPWPASDRKKSECAF 115
 | || | : : |||| | |||| | : : | | | | | : : |
 Db 48 HFKGQAQNYSTLLLEEASARLLVGARGALFSLSANDIGDGAHKE-IHWEASPEMQSKCHQ 106
 Qy 116 KKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQ 175
 | | : | : | : || : | | |||| || | | | : : : || | : || :
 Db 107 KGKNNQTECFNHVRFLQRLNSTHLYACGTHAFQPLCAAID-AEAFTLPTSFE---EGKEK 162
 Qy 176 SPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFV- 234


```

      | : || |   | : : || || : |   | | : | :   :   :   | | : || ||
Db      163 CPYDPARGFTGLIIDGGLYTATRYEF-RSIPDIRRSRHPHSLRTEETPMHWL-NDAEFVF 220
Qy      235 -----AAIPSTQVVYFFFEETASE-----FDDFERLH-TSRVARVCKNDVGGEKLL 279
      : | :   || : || | | : |   |   |   : || || || | : || : | : |
Db      221 SVLVRESKASAVGDDDDKVYFFTERATEEGSGSFTQSRSSHRVARVARVCKGDLGGKKIL 280
Qy      280 QKKWTTFLKAQLLCTQPQQLPFNVIRHAVLLPADSPTAPIYAVFT--SQWQVGGTRSSA 337
      || || | : || | : | |   :   : | | : : | | | | : || :   : ||
Db      281 QKKWTSFLKARLICHIP---LYETLRGVCSLDAETSSRTHFYAAFTLSTQWKT--LEASA 335
Qy      338 VCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDK----- 387
      : | : | : | : || | | |   : || | | | | || || | | : | :
Db      336 ICRYDLAEIQAVFAGPYMEYQDGSRRWGRYEGGVPEPRPGSCITDSLRSQGYNSSQDLPS 395
Qy      388 -ALTFMKDHFLLMDEQVV---GTPLLKSGVEYTRLAVETAQGLDGHSHLVMYLGTTTGSL 443
      | | : | | | | | | | | | | : | | | | | | | | : : : : || | | :
Db      396 LVLDFVKLHPLMARPVVPTRGRLLLKRNIRYTHLTGTPVTTAGPTYDLLFLGTADGWI 455
Qy      444 HKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVYES 503
      || || | | | : || | | : : | | | : | : || | | : || : || | | |
Db      456 HKAVVLG-SGMHIIETQVFRESQSVENLVISLLQHSLYVGAPSGVIQLPLSSCSRYRSC 514
Qy      504 VDCVLARDPHCAWDPESTRCCLL-----SAPNLNSWKQDMERGNPEWACASGPMSRSLR 557
      || : || || | : || | | | | | | | : : | | : || | | | | | |
Db      515 YDCILARDPYCGWDPGTHACAAATTIANRSQGSRTALIQDIERGNR--GCES---SRDTG 569
Qy      558 PQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDG 617
      | | | : |   :   : || | | | | | | | | | | | : || | : | | |
Db      570 P---PPPLKTRSVLRGDDVLLPCDQPSNLRALW-----LLNGSMGL--SDG 611
Qy      618 VGGL-----YQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPR 658
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      612 QGGYRVGVDGLLVTDAPQPEHSGNYGCYAEENGLRTL LASYSLTVRPATPAPAPKAPATP- 670
Qy      659 EHVKVPLTRVSGGAALAAQQSYWPHFVTVTVL FALVLSGALIILVASPL----- 707
      || || | | | | | | | | | | | | | | | | | | | | | | | |
Db      671 -----GAQLAPD-----VRLLYVLAIAALGGLCLILASSLLYVACLREGRR 711
Qy      708 -----RALRARGKVQGCETLR---PGEK 727
      || || | | | : | : | | | :
Db      712 GRRRKYSLGRASRAGGSAVQLQTVSGQCPGEE 743

```

RESULT 12

US-09-854-845-49

; Sequence 49, Application US/09854845

; Patent No. 6750054

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Wang, Xiaoming

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0177-USA

; CURRENT APPLICATION NUMBER: US/09/854,845

Query Match		22.2%;	Score 895;	DB 4;	Length 766;
Best Local Similarity		33.2%;	Pred. No. 3.7e-80;		
Matches		245;	Conservative 101;	Mismatches 243;	Indels 148; Gaps 27;
Qy	110	KSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKV	169		
Db	2	QSKCHQKGKNNQTECFNHVRFLQRLNSTHLYACGTHAFQPLCAAID-AEAFTLPTSFE--	58		
Qy	170	MEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHH	229		
Db	59	-EGKEKCPYDPARGFTGLIIDGGLYTATRYEF-RSIPDIRSRHPHSLRTEETPMHWL-N	115		
Qy	230	DASFV-----AAIPSTQVVYFFFEETASE-----FDFFERLH-TSRVARVCKNDV	273		
Db	116	DAEFVFSVLVRESKASAVGDDDKVYYFFTERATEEGSGSFTQSRSSHRVARVARVCKGDL	175		
Qy	274	GGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFT--SQWQVG	331		
Db	176	GGKKILQKKWTSFLKARLICHIP---LYETLRGVCSLDAETSSRTHFYAAFTLSTQWKT-	231		
Qy	332	GTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSS	385		
Db	232	-LEASAIcryDLAEIQAVFAGPYMEYQDGSRRWGRYEGGVPEPRPGSCITDSLRSQGYNS	290		
Qy	386	DK-----ALTFMKDHFLLMDEQVV---GTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLG	437		
Db	291	SQDLPSLVLDVFKLHPLMARPVVPTRGRPLLLKRNIRYTHLTGTPVTTTPAGPTYDLLFLG	350		
Qy	438	TTTGS LHKAVVSGDSSAHLVEEIQLFDPDPEPV RN LQLAPTQGA V FVGFSGGVWRVPRANC	497		
Db	351	TADGWIHKAVVLG-SGMHII EETQVFRESQSVENLVISLLQHS LYVGAPSGVIQLPLSSC	409		
Qy	498	SVYESCVDCVLARDPHCAWD PESRTCCLLSA-PNLNSWKQDMERGNPEWACASGPMSRSL	556		
Db	410	SRYRSCYDCILARDPYCGWDPGTHACAAATTIANRTALIQDIERGNR--GCES---SRDT	464		
Qy	557	RPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQD	616		
Db	465	GP---PPPLKTRSVLRGDDVLLPCDQPSNLARALW-----LLNGSMGL--SD	506		
Qy	617	GVGGL-----YQCWATENGFSYPVISYWVDSQDQTLALDPELAGIP	657		
Db	507	GOGGYRVGVGDGLLVTDAPPEHSGNYGCGYAEENGLRTL LASYSLTVRPATPAPAPKAPATP	566		

```

Qy      658 REHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAVLVLSGALIILVASPL----- 707
          || ||           | : : | : | | : : || |
Db      567 -----GAQLAPD-----VRLLYVLAIAALGGLCLILASSLLYVACLREGR 606

Qy      708 -----RALRARGKVQGCE-----LRPGEKAPLS-----REQHLQSP 739
          || || |       :|           : | :| |           \ | : | |
Db      607 RGRRRKYSLGRASRAGGSQVQLQTVSGRALQVHMGSMSPPSAWPCVLDGPETRQVLCQPP 666

Qy      740 KECRTSASDQDADNNCL 756
          | | | : : | |
Db      667 KPCVHSHAHME---ECL 680

```

RESULT 13

US-09-854-845-25

```

; Sequence 25, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 697
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-25

```

```

Query Match          22.2%; Score 893; DB 4; Length 697;
Best Local Similarity 36.3%; Pred. No. 5.1e-80;
Matches 225; Conservative 90; Mismatches 209; Indels 96; Gaps 23;

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Qy      57 HQKG-LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRPKNMIPWPASDRKKSECAF 115
          | || | : : |||| | |||| | : : | | | | | | : : |
Db      48 HFKGQAQNYSTLLLEEASARLLVGARGALFSLSANDIGDGAHKE-IHWEASPEMQSKCHQ 106

Qy     116 KKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQ 175
          | | : : | : || | | | |||| || | | | | : : : || | : || | :
Db     107 KGKNNQTECFNHVRFLQRLNSTHLYACGTHAFQPLCAAID-AEAFTLPTSFE---EGKEK 162

Qy     176 SPFDPAHKHHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFV- 234
          | : || | | : : || || : | | | | : | : : : || : || ||
Db     163 CPYDPARGFTGLIIDGGLYTATRYEF-RSIPDIRRSRPHSLRTEETPMHWL-NDAEFVF 220

Qy     235 -----AAIPSTQVVYFFFEETASE-----FDFFERLH-TSRVARVCKNDVGGEKLL 279
          : | : | | : || | | : | | | : || || || | : || : | : |

```

Db 221 SVLVRESKASAVGDDDKVYYFFTERATEEGSGSFTQSRSSHRVARVARVCKGDLGGKKIL 280
 Qy 280 QKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFT--SQWQVGGTRSSA 337
 |||||:||||:|:| | : :| | |:: : | || || :||: :||
 Db 281 QKKWTSFLKARLICHIP---LYETLRGVCSLDAETSSRTHFYAAFTLSTQWKT--LEASA 335
 Qy 338 VCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDK----- 387
 :| : | :|: || | | | : || | | | ||||| | | :| :
 Db 336 ICRYDLAEIQAVFAGPYMEYQDGSRRWGRYEGGVPEPRPGSCITDSLRSQGYNSSQDLPS 395
 Qy 388 -ALTFMKDHFMLDEQVV---GTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTTTGS 443
 | | :| | || | | | |||:| : || | | : : :||| | :
 Db 396 LVLDVFKLHPLMARPVVPTGRPLLLKRNIRYTHLTGTPVTTPAGPTYDLLFLGTADGWI 455
 Qy 444 HKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVYES 503
 ||||| | | |::|| |:| : : | || : : | :|| | | :|| :|| | ||
 Db 456 HKAVVLG-SGMHIEETQVFRESQSVENLVISLLQHSLYVGAPSGVIQLPLSSCSRYRSC 514
 Qy 504 VDCVLARDPHCAWDPESTRCCLLSA-PNLNSWKQDMERGN----- 542
 ||:|||||:| ||| : | : | : ||:||||
 Db 515 YDCILARDPYCGWDPGTHACAAATTIANRTALIQDIERNRGCESSRDTGRALQVHM GSM 574
 Qy 543 ---PEWACA-SGPMRSRLRPQ-SRPQI-----IKEVLAVPNSILELPCPHL----- 583
 | | || :| : | :| : :|| : | : | ||
 Db 575 SPPSAWPCVLDGPETRQVLCQPPKPCVHSHAHMEECLSAG---LQCPHPLLHLLVHSCFIP 631
 Qy 584 -----SALASYWWSHGPA 596
 | | || ||
 Db 632 ASGLGVPSQLPHPIWSSSPA 651

RESULT 14

US-09-854-845-45

; Sequence 45, Application US/09854845

; Patent No. 6750054

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Wang, Xiaoming

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6750054e1 Human Semaphorin Homologs and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0177-USA

; CURRENT APPLICATION NUMBER: US/09/854,845

; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: US 60/205,274

; PRIOR FILING DATE: 2000-05-18

; PRIOR APPLICATION NUMBER: US 60/208,893

; PRIOR FILING DATE: 2000-06-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 45

; LENGTH: 739

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-854-845-45

Qy	110	KSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKV	169
Db	2	QSKCHQKGKNNQTECFNHVRFLQRLNSTHLYACGTHAFQPLCAAID-AEAFTLPTSFE--	58
Qy	170	MEGKGQSPFPDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHH	229
Db	59	-EGKEKCPYDPARGFTGLIIDGGLYTATRYEF-RSIPDIRRSRHPHSLRTEETPMHWL-N	115
Qy	230	DASFV-----AAIPSTQVVYFFFEETASE-----FDDFERLH-TSRVARVCKNDV	273
Db	116	DAEFVFSVLVRESKASAVGDDDKVYFFTERATEEGSGSFTQSRSSHRVARVARVCKGDL	175
Qy	274	GGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFT--SQWQVG	331
Db	176	GGKKILQKKWTSFLKARLICHIP---LYETLRGVCSLDAETSSRTHFYAAFTLSTQWKT-	231
Qy	332	GTRSSAVCAFSLLDIERVFKGYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSS	385
Db	232	-LEASAICRYDLAEIQAVFAGPYMEYQDGSRRWGRYEGGVPEPRPGSCITDSLRSQGYNS	290
Qy	386	DK-----ALTFMKDHFMLDEQVV---GTPLLKSGVEYTRLAVETAQGLDGHSHLVMYLG	437
Db	291	SQDLPSLVLDVFKLHPLMARPVVPTGRGRPLLLKRNIRYTHLTGTPVTTTAPGPTYDLLFLG	350
Qy	438	TTTGSLLHKAVVSGDSSAHLVEEIQLFDPDEPVNRNLQLAPTQGAVFVGFSGGVWRVPRANC	497
Db	351	TADGWIHKAVVLG-SGMHIIETQVFRESQSVENLVISLLQHSLYVGAPSGVIQLPLSSC	409
Qy	498	SVYESCVDCVLARDPHCAWDPEsrTCCLLSA-PNLNSWKQDMERGNPEWACASGPMsrSL	556
Db	410	SRYRSCYDCILARDPYCGWDPGTHACAAATTIANRTALIQDIERNR--GCES---SRDT	464
Qy	557	RPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQD	616
Db	465	GP---PPPLKTRSVLRGDDVLLPCDQPSNLARALW-----LLNGSMGL--SD	506
Qy	617	GVGGL-----YQCWATENGFSYPVISYWVDSQDQTLALDPELAGIP	657
Db	507	GQGGYRVGVDGLLVTDQPEHSGNYGCTAEENGLRLLASYSLTVRPATPAPAPKAPATP	566
Qy	658	REHVKVPLTRVSGGAALAAQSYWPHFVTVTVLFAVLVSGALIILVASPL-----	707
Db	567	-----GAQLAPD-----VRLLYVLAIAALGGLCLILASSLLYVACLREGR	606
Qy	708	-----RALRARGKVQGCETLR---PGEK	727
Db	607	RGRRRKYSILGRASRAGGSAVQLQTVSGQCPGEE	639

RESULT 15
US-09-854-845-47
; Sequence 47, Application US/09854845
; Patent No. 6750054

```
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054e1 Human Semaphorin Homologs and
Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 771
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-47
```

```
Query Match          22.0%; Score 888.5; DB 4; Length 771;
Best Local Similarity 33.0%; Pred. No. 1.7e-79;
Matches 245; Conservative 101; Mismatches 243; Indels 153; Gaps 27;
```

```
Qy      110 KSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKV 169
          :|:| | |:|:|:| | | :| | | | | | | | | | : : : | | :
Db      2   QSKCHQKGKNNQTECFNHVRFLQRLNSTHLYACGTHAFQPLCAAID-AEAFTLPTSFE-- 58

Qy      170 MEGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHH 229
          ||| : |:| | | : : | | | : | | | : | : : : | | :
Db      59 -EGKEKCPYDPARGFTGLIIDGGLYTATRYEF-RSIPDIRRSRHPHSLRTEETPMHWL-N 115

Qy      230 DASFV-----AAIPSTQVVYFFFEETASE-----FDDFERLH-TSRVARVCKNDV 273
          || || : | : | | | | | | | | | | | | : | | | | | | :
Db      116 DAEFVFSVLVRESKASAVGDDDKVYFFTERATEEGSGSFTQSRSSHRVARVARVCKGDL 175

Qy      274 GGEKLLQKKWTTFLKAQLLCTQPQQLPFNVIRHAVLLPADSPTAPHIYAVFT--SQWQVG 331
          ||:|:| | | | | | | | | | | | : : | | | | | | : | | :
Db      176 GGKKILQKKWTSFLKARLICHIP---LYETLRGVCSLDAETSSRTHFYAAFTLSTQWKT- 231

Qy      332 GTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSS 385
          :|:|:| : | :|: | | | | | : | | | | | | | | | | | :|
Db      232 -LEASAICRYDLAEIQAVFAGPYMEYQDGSRRWGRYEGGVPEPRPGSCITDSLRSQGYNS 290

Qy      386 DK-----ALTFMKDHFLMDEQVV---GTPLLKSGVEYTRLAVETAQGLDGHSHLVMYL 437
          : | |:| | | | | | | | | | | | | | | | | | : : : | |
Db      291 SQDLPSLVLDVFKLHPLMARPVVPTGRPLLLKRNIRYTHLTGTPVTTTPAGPTYDLLFLG 350

Qy      438 TTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANC 497
          | | :| | | | | | | :| | | : : | | | : : | | | : | :| :|
Db      351 TADGWIHKAVVLG-SGMHIIETQVFRESQSVENLVISLLQHSLYVGAPSGVIQLPLSSC 409

Qy      498 SVYESCVDCVLARDPHCAWDPESTRCCLL-----SAPNLNSWKQDMERGNPEWACASGP 551
          | | | | |:| | | | | | | | | | : | | : : | | : | | | | |
Db      410 SRYRSCYDCILARDPYCGWDPGTHACAAATTIANRSQGSRTALIQDIERNR--GCES-- 465
```

Qy	552	MSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLL	611
		: : : : :	
Db	466	-SRDTGP---PPPLKTRSVLRGDDVLLPCDQPSNLRALW-----LLNGSMG	508
Qy	612	LIVQDGVGGL-----YQCWATENGFSYPVISYWVDSQDQTLALDPE	652
		: : : : :	
Db	509	L--SDGQGGYRVGVGDGLLVTDAPQPEHSGNYGCYAEENGLRTL LASYSLTVRPATPAPAPK	566
Qy	653	LAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPL-----	707
		: : : ::	
Db	567	APATP-----GAQLAPD-----VRLLYVLAIAALGGLCLILASSLLYVAC	606
Qy	708	-----RALRARGKVQGCET-----LRPGEKAPLS-----REQ	734
		: : : :	
Db	607	LREGRRGRRRKYSLGRASRAGGSQVQLQTVSGRALQVHMGSMSPPSAWPCVLDGPETRQV	666
Qy	735	HLQSPKECRTSASDQDADNNCL	756
		: ::	
Db	667	LCQPPKPCVHSHAHME---ECL	685

Search completed: February 10, 2005, 02:18:27
Job time : 60 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 02:09:18 ; Search time 44 Seconds
(without alignments)
1664.113 Million cell updates/sec

Title: US-10-015-391A-277
Perfect score: 4031
Sequence: 1 MALPALGLDPWSLLGLFLFQ.....CRTSASDVDADNNCLGTEVA 761

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3280.5	81.4	760	2	I48745	semaphorin B - mou
2	1198.5	29.7	782	2	I48746	semaphorin C - mou
3	1079.5	26.8	834	2	S66498	M-sema F protein p
4	838.5	20.8	753	2	G02173	semaphorin III fam
5	838	20.8	772	2	A49069	collapsin - chicke
6	836	20.7	772	2	I48747	semaphorin D - mou
7	825.5	20.5	771	2	D49423	semaphorin III pre
8	820	20.3	749	2	G01856	semaphorin V - hum
9	802.5	19.9	751	2	I48748	semaphorin E - mou
10	784.5	19.5	748	2	I48744	semaphorin A - mou
11	766	19.0	666	2	I58169	semaphorin III - m
12	677.5	16.8	1074	2	JC5928	semaphorin F precu
13	657.5	16.3	730	2	JH0798	fasciclin IV precu

14	641	15.9	1011	2	JC8059	semaphorin 6D-1 -
15	621.5	15.4	712	2	T27165	hypothetical prote
16	609.5	15.1	711	2	A49423	semaphorin I precu
17	605.5	15.0	656	2	B49423	semaphorin I - fru
18	600.5	14.9	724	2	C49423	semaphorin II prec
19	442.5	11.0	653	2	T03102	semaphorin homolog
20	350	8.7	676	2	T33853	hypothetical prote
21	281.5	7.0	1905	2	I51553	Plexin - African c
22	277	6.9	1872	2	JC4976	plexin 3 precursor
23	262	6.5	1894	2	JC4980	plexin 1 precursor
24	238	5.9	1884	2	JC4975	plexin 2 precursor
25	228	5.7	2051	2	T13164	plexin B - fruit f
26	225.5	5.6	1945	2	T13937	plexin A - fruit f
27	157	3.9	1806	2	T23298	hypothetical prote
28	151.5	3.8	1568	2	T09074	semaphorin recepto
29	146.5	3.6	403	2	E42521	A39R protein - vac
30	145	3.6	441	2	S29921	hypothetical prote
31	139.5	3.5	866	2	T06454	probable lipoxigen
32	132.5	3.3	317	2	T46426	hypothetical prote
33	132.5	3.3	1375	1	JC5148	hepatocyte growth
34	128.5	3.2	446	2	AI1253	glutathione reduct
35	127.5	3.2	1369	1	JC4860	protein-tyrosine k
36	127	3.2	1425	2	T30811	hepatocyte growth
37	121	3.0	1374	2	T30809	plasminogen relate
38	120	3.0	868	2	T06827	lipoxxygenase (EC 1
39	119	3.0	1400	1	I38185	protein-tyrosine k
40	116	2.9	2126	2	H70621	probable polyketid
41	114	2.8	295	2	JQ1775	SalL9R protein - v
42	114	2.8	861	1	S01142	lipoxxygenase (EC 1
43	114	2.8	862	2	T07775	lipoxxygenase (EC 1
44	114	2.8	3573	2	S23070	erythronolide synt
45	112.5	2.8	862	2	S57964	lipoxxygenase (EC 1
46	111.5	2.8	1378	1	I48751	protein-tyrosine k
47	110.5	2.7	446	2	AG1616	glutathione reduct
48	110	2.7	2767	1	UIHU	thyroglobulin prec
49	108.5	2.7	413	2	E82312	phage integrase VC
50	107.5	2.7	813	2	F83476	probable sideropho
51	107.5	2.7	1379	1	S01254	hepatocyte growth
52	107	2.7	868	2	S56655	lipoxxygenase (EC 1
53	106.5	2.6	570	2	D72597	hypothetical prote
54	106	2.6	3519	2	S43048	polyketide synthas
55	105	2.6	570	2	T33320	hypothetical prote
56	103.5	2.6	829	2	B86467	hypothetical prote
57	103	2.6	525	2	T50893	methoxyneurosporen
58	102.5	2.5	657	2	S25184	cspl protein - Cor
59	102.5	2.5	1218	2	S38182	probable transport
60	102.5	2.5	1404	1	A48196	protein-tyrosine k
61	102	2.5	1375	2	T30813	plasminogen relate
62	101	2.5	753	2	B96687	subtilisin-like pr
63	100.5	2.5	876	2	T07101	lipoxxygenase (EC 1
64	99.5	2.5	864	2	S13381	lipoxxygenase (EC 1
65	99	2.5	2100	2	T03223	probable polyketid
66	98	2.4	753	2	T01619	hypothetical prote
67	98	2.4	856	2	T06596	lipoxxygenase (EC 1
68	98	2.4	876	2	T05943	probable lipoxxygen
69	98	2.4	1310	1	WZBE62	gene 62 protein -
70	97.5	2.4	741	2	S18906	lipoxxygenase (EC 1

71	97.5	2.4	865	1	DASYL1	lipoxygenase (EC 1
72	97.5	2.4	898	2	T14764	hypothetical prote
73	97.5	2.4	1158	2	T50454	probable rho1 GDP-
74	97.5	2.4	1238	2	S68700	HPTP beta-like tyr
75	97	2.4	590	2	D69722	thiamin biosynthes
76	97	2.4	599	2	S18612	lipoxygenase (EC 1
77	97	2.4	1621	2	S62356	TRP-185 protein -
78	96.5	2.4	2215	2	T00348	LR11 protein - mou
79	96	2.4	499	2	S01038	transcription fact
80	96	2.4	605	2	JC5239	insulin-like growt
81	95.5	2.4	666	2	C84861	hypothetical prote
82	95.5	2.4	4568	2	T08030	dynein beta heavy
83	95	2.4	1015	2	S55474	Human giant larvae
84	95	2.4	2338	2	T25810	hypothetical prote
85	95	2.4	4391	2	A38096	perlecan precursor
86	94.5	2.3	475	2	S74684	isocitrate dehydro
87	94.5	2.3	1277	2	T30532	neural cell adhesi
88	94	2.3	955	2	T39765	probable nuclear m
89	94	2.3	1478	2	S20117	protein kinase BCK
90	94	2.3	2629	2	T30987	telomerase-associa
91	94	2.3	2769	1	UIBO	thyroglobulin prec
92	93.5	2.3	285	2	F82957	hypothetical prote
93	93.5	2.3	507	2	S46500	cellulase (EC 3.2.
94	93.5	2.3	546	2	C72453	hypothetical prote
95	93.5	2.3	832	2	AE1492	hypothetical prote
96	93.5	2.3	865	1	S23454	lipoxygenase (EC 1
97	93	2.3	576	2	S50113	coilin, p80 - huma
98	93	2.3	917	2	T04661	hypothetical prote
99	93	2.3	1067	2	E81051	multiple transfera
100	93	2.3	1711	2	AD1842	WD-40 repeat prote
101	92.5	2.3	599	1	H65057	sulfite reductase
102	92.5	2.3	809	2	T40574	guanine nucleotide
103	92.5	2.3	866	1	S59872	replication licens
104	92.5	2.3	890	2	T34243	hypothetical prote
105	92.5	2.3	1479	2	T42710	mannose receptor,
106	92.5	2.3	2150	2	T08165	RNA1 polyprotein -
107	92.5	2.3	2944	2	A54849	collagen alpha 1(V
108	92	2.3	490	2	F87443	conserved hypothet
109	92	2.3	857	2	S01864	lipoxygenase (EC 1
110	92	2.3	1273	2	E72611	probable ATP-depen
111	91.5	2.3	528	2	C87663	conserved hypothet
112	91.5	2.3	631	2	A57286	probable serine/th
113	91.5	2.3	859	1	JQ2267	lipoxygenase (EC 1
114	91	2.3	540	2	S72233	transcription fact
115	91	2.3	627	2	S50583	hypothetical prote
116	91	2.3	861	2	S44940	lipoxygenase (EC 1
117	91	2.3	1010	2	D72203	hypothetical prote
118	91	2.3	1228	2	S60085	nitrate reductase
119	90.5	2.2	349	2	A53340	interferon regulat
120	90.5	2.2	457	2	A27449	T-cell surface gly
121	90.5	2.2	732	2	B90975	hypothetical prote
122	90.5	2.2	1535	2	S46224	peroxidase - frui
123	90.5	2.2	2569	2	T14164	peptide synthetase
124	90	2.2	608	2	C97575	glutamine-fructose
125	90	2.2	608	2	AC2796	hypothetical prote
126	90	2.2	839	2	T06354	lipoxygenase (EC 1
127	90	2.2	853	2	T07662	lipoxygenase (EC 1

128	90	2.2	1004	2	T38074	hypothetical prote
129	90	2.2	1217	2	T00270	hypothetical prote
130	90	2.2	1422	2	T24212	hypothetical prote
131	89.5	2.2	259	2	PS0102	genome polyprotein
132	89.5	2.2	409	2	S12588	pol polyprotein -
133	89.5	2.2	567	2	A70603	hypothetical prote
134	89.5	2.2	615	2	D70907	hypothetical prote
135	89.5	2.2	1041	2	S55862	probable membrane
136	89.5	2.2	2163	2	T15276	hypothetical prote
137	89.5	2.2	3649	1	S18268	delta-(L-alpha-ami
138	89	2.2	375	2	JX0131	cellulase (EC 3.2.
139	89	2.2	452	1	I37565	transforming prote
140	89	2.2	489	2	B33416	nuclear factor I -
141	89	2.2	847	2	A56039	GTPase-activating
142	89	2.2	875	2	C81209	tspA protein NMB03
143	89	2.2	954	2	I61714	co-repressor prote
144	89	2.2	1337	2	T13948	atypical protein k
145	88.5	2.2	217	1	JC2557	metalloproteinase
146	88.5	2.2	373	2	E85757	probable efflux pu
147	88.5	2.2	373	2	G90861	probable efflux pu
148	88.5	2.2	468	2	C82722	UDP-N-acetylmuramo
149	88.5	2.2	495	2	C95144	glucose-6-phosphat
150	88.5	2.2	495	2	A98012	glucose-6-phosphat
151	88.5	2.2	599	2	C91081	sulfite reductase
152	88.5	2.2	599	2	D85926	sulfite reductase
153	88.5	2.2	839	1	DASYL2	lipxygenase (EC 1
154	88.5	2.2	935	2	T40715	hypothetical prote
155	88.5	2.2	975	2	T48107	hypothetical prote
156	88.5	2.2	1405	2	H87230	probable integral
157	88.5	2.2	1440	2	T44872	probable integral
158	88.5	2.2	2326	2	B47447	calcium channel pr
159	88.5	2.2	2453	2	S60254	nuclear receptor c
160	88.5	2.2	2605	2	T18552	saframycin Mx1 syn
161	88.5	2.2	4969	2	A37113	ryanodine receptor
162	88	2.2	466	2	B70538	probable glucose-6
163	88	2.2	475	2	A97289	para-aminobenzoate
164	88	2.2	651	2	AE3230	hydantoin utilizat
165	88	2.2	652	2	AH2245	thiamin biosynthes
166	88	2.2	654	2	B55579	biotin carboxyl ca
167	88	2.2	695	2	B75295	hypothetical prote
168	88	2.2	949	2	E71940	translation initia
169	88	2.2	1129	2	T42732	A-kinase anchoring
170	88	2.2	1548	2	S54723	UDP-glucose-glycop
171	88	2.2	1865	2	G86152	T7I23.15 protein -
172	88	2.2	2723	2	T03221	probable polyketid
173	88	2.2	4861	2	S71752	giant protein p619
174	87.5	2.2	304	2	E83052	tRNA pseudouridine
175	87.5	2.2	422	2	F86581	CHLPN 76 kDa homol
176	87.5	2.2	422	2	E72042	conserved hypothet
177	87.5	2.2	802	2	T45642	FtsH metalloprotei
178	87.5	2.2	815	2	T00538	probable serine pr
179	87.5	2.2	823	2	F85624	hypothetical prote
180	87.5	2.2	843	1	GNVWK	pol polyprotein -
181	87.5	2.2	3587	2	T31075	tyrocidine synthet
182	87	2.2	372	2	S69246	lignin peroxidase
183	87	2.2	372	2	A32322	lignin peroxidase
184	87	2.2	452	1	S17403	transforming prote

185	87	2.2	726	2	T34638	hypothetical prote
186	87	2.2	948	2	C75265	hexagonally packed
187	87	2.2	1639	2	T14181	peptide synthetase
188	86.5	2.1	342	2	T23224	hypothetical prote
189	86.5	2.1	391	2	AG2318	hypothetical prote
190	86.5	2.1	547	2	B96530	Similar to CCS1 [i
191	86.5	2.1	739	2	B88553	protein K04H4.2b [
192	86.5	2.1	823	2	A90761	hypothetical prote
193	86.5	2.1	1189	2	JC6118	SH2-containing ino
194	86.5	2.1	1390	2	T30346	insulin receptor -
195	86.5	2.1	1562	2	T43022	ATP-binding multid
196	86.5	2.1	1575	2	T18545	lysobactin synthet
197	86.5	2.1	3635	2	T10053	laminin alpha 5 ch
198	86.5	2.1	4735	2	T17463	rifamycin polyketi
199	86	2.1	335	2	T48995	hypothetical prote
200	86	2.1	372	2	S01028	lignin peroxidase
201	86	2.1	399	2	JC4215	T-cell reactive pr
202	86	2.1	443	2	T31101	probable phosphoma
203	86	2.1	541	2	T46423	hypothetical prote
204	86	2.1	620	2	T30765	hypothetical prote
205	86	2.1	723	2	AI1290	beta-glucosidases
206	86	2.1	723	2	C83412	probable ATP-bindi
207	86	2.1	775	1	WMBE19	ribonucleoside-dip
208	86	2.1	816	2	T08978	serine proteinase
209	86	2.1	1004	2	D71490	probable exodeoxyr
210	86	2.1	1058	2	T30580	P-type ATPase - sl
211	86	2.1	1067	2	G81825	probable drug effl
212	86	2.1	1161	2	G81915	hypothetical prote
213	86	2.1	1332	2	D84669	aldehyde oxidase [
214	86	2.1	1511	2	T42711	sulfonylurea recep
215	86	2.1	1811	2	T00035	nonstructural poly
216	86	2.1	1827	2	B70984	probable polyketid
217	86	2.1	7962	2	I38346	elastic titin - hu
218	85.5	2.1	194	2	E75510	hypothetical prote
219	85.5	2.1	407	2	E86167	protein F21B7.29 [
220	85.5	2.1	506	2	A33416	nuclear factor I -
221	85.5	2.1	509	2	T03275	probable cytochrom
222	85.5	2.1	510	2	F75260	glutamyl-tRNA(Gln)
223	85.5	2.1	753	2	T05649	hypothetical prote
224	85.5	2.1	823	2	B85822	hypothetical prote
225	85.5	2.1	956	2	H81654	conserved hypothet
226	85.5	2.1	1072	2	T37742	serine threonine-p
227	85.5	2.1	2205	1	GNNY2W	genome polyprotein
228	85.5	2.1	3534	2	T42567	tegument protein 2
229	85.5	2.1	4869	2	S66572	ryanodine receptor
230	85.5	2.1	4967	2	S72269	ryanodine receptor
231	85	2.1	372	2	JT0402	lignin peroxidase
232	85	2.1	454	2	AE1244	acetyl-CoA carboxy
233	85	2.1	583	1	A25937	arsenical pump-dri
234	85	2.1	596	2	T23685	hypothetical prote
235	85	2.1	601	2	T15260	hypothetical prote
236	85	2.1	631	2	T35234	probable secreted
237	85	2.1	640	2	T08758	hypothetical prote
238	85	2.1	660	2	T02755	fanconi anemia com
239	85	2.1	685	2	C56591	E75 B steroid rece
240	85	2.1	749	2	G86186	hypothetical prote
241	85	2.1	853	2	T07036	lipxygenase (EC 1

242	85	2.1	858	2	T12142	lipoxxygenase (EC 1
243	85	2.1	1043	2	T19734	hypothetical prote
244	85	2.1	1057	2	I38171	hugl protein - hum
245	85	2.1	1172	2	A42587	thrombospondin 2 p
246	85	2.1	1349	2	T01699	aldehyde oxidase (
247	85	2.1	1777	2	T00490	nonstructural prot
248	85	2.1	2395	1	S50820	surface protein ty
249	84.5	2.1	278	2	H70806	hypothetical prote
250	84.5	2.1	385	2	E83414	conserved hypothet
251	84.5	2.1	471	2	S76290	hypothetical prote
252	84.5	2.1	482	2	D97162	UDP-N-acetylmuramy
253	84.5	2.1	580	2	C81352	lipid export ABC t
254	84.5	2.1	595	2	JQ1684	anthranilate synth
255	84.5	2.1	627	2	AB0535	hypothetical prote
256	84.5	2.1	712	2	G02512	interleukin-1 rece
257	84.5	2.1	737	2	S72442	actin-fragmin kina
258	84.5	2.1	760	2	T39991	minichromosome mai
259	84.5	2.1	1027	2	I38604	p53-binding protei
260	84.5	2.1	1102	2	AD2136	microcystin synthe
261	84.5	2.1	1204	2	S70393	pol polyprotein -
262	84.5	2.1	1346	2	T17412	polyketide synthas
263	84.5	2.1	1394	2	T34061	hypothetical prote
264	84.5	2.1	1559	2	AI2348	ferredoxin-glutama
265	84.5	2.1	1743	2	T26859	hypothetical prote
266	84.5	2.1	2104	2	D91286	hypothetical prote
267	84.5	2.1	2104	2	H86127	hypothetical prote
268	84.5	2.1	3623	2	T08618	intrinsic factor-B
269	84	2.1	263	2	I37533	MHC class II histo
270	84	2.1	286	2	A85739	probable dehydroge
271	84	2.1	286	2	H90879	probable dehydroge
272	84	2.1	444	2	T42537	probable transketo
273	84	2.1	454	2	AG1977	hypothetical prote
274	84	2.1	560	2	S51684	glutamate-tRNA lig
275	84	2.1	590	1	TVFFDS	protein-tyrosine k
276	84	2.1	627	2	T10290	hypothetical prote
277	84	2.1	695	2	A38314	L-amino-acid oxida
278	84	2.1	781	2	H95392	probable MrcB peni
279	84	2.1	886	2	A59223	nitrate reductase
280	84	2.1	917	2	I48950	telencephalin prec
281	84	2.1	939	2	C70876	hypothetical prote
282	84	2.1	1506	2	JC5985	phosphoinositide 3
283	84	2.1	3229	2	S27852	probable cell-surf
284	84	2.1	4845	2	T31067	BIR repeat contain
285	84	2.1	5327	2	T13564	microtubule-associ
286	83.5	2.1	373	2	T02976	probable DNA bindi
287	83.5	2.1	469	2	A55484	p52(Shc) protein -
288	83.5	2.1	480	2	A48043	ubiquinol-cytochro
289	83.5	2.1	508	2	S19266	anthranilate synth
290	83.5	2.1	568	2	T28041	hypothetical prote
291	83.5	2.1	581	2	E84582	malate oxidoreduct
292	83.5	2.1	592	2	D97171	uncharacterized co
293	83.5	2.1	595	2	A42086	CD30 antigen precu
294	83.5	2.1	640	2	S49932	MET30 protein - ye
295	83.5	2.1	748	2	S66129	disintegrin (EC 3.
296	83.5	2.1	777	1	WMAD41	late 100K protein
297	83.5	2.1	864	1	S07075	lipoxxygenase (EC 1
298	83.5	2.1	886	2	A82825	aconitate hydratase

299	83.5	2.1	1153	2	T31080	nitric-oxide synth
300	83.5	2.1	1191	2	S76414	beta transducin-li
301	83.5	2.1	1210	2	T07658	aldehyde oxidase (
302	83.5	2.1	1317	2	T03748	apoptosis associat
303	83.5	2.1	1609	2	E87243	probable cation tr
304	83.5	2.1	2132	1	A55182	aggreCAN precursor
305	83	2.1	261	2	S17889	class II histocomp
306	83	2.1	286	2	A48399	probable oxidoredu
307	83	2.1	395	2	B75520	probable lipopolys
308	83	2.1	428	2	I57486	pregnancy-specific
309	83	2.1	428	2	JS0032	pregnancy-specific
310	83	2.1	436	2	H69588	acetylornithine de
311	83	2.1	480	2	C86174	hypothetical prote
312	83	2.1	481	2	E97219	rieske FeS-domain
313	83	2.1	519	2	T45764	hypothetical prote
314	83	2.1	525	2	S19701	hypothetical prote
315	83	2.1	548	2	E70546	hypothetical prote
316	83	2.1	549	2	A39345	alpha-mannosidase
317	83	2.1	691	2	D90592	hypothetical prote
318	83	2.1	836	2	S54152	sepB protein - Eme
319	83	2.1	842	2	T32258	hypothetical prote
320	83	2.1	864	2	T05945	lipooxygenase (EC 1
321	83	2.1	880	2	G81786	Neisseria-specific
322	83	2.1	1077	2	D90387	peptidase related
323	83	2.1	1287	2	A43488	genome polyprotein
324	83	2.1	1375	2	JT0345	dextran sucrose (EC
325	83	2.1	1427	2	I51669	tumor suppressor -
326	83	2.1	1762	2	T09245	genome polyprotein
327	83	2.1	2124	2	A28452	proteoglycan core
328	83	2.1	2265	1	FNBO	fibronectin - bovi
329	83	2.1	2450	2	S71625	protein-tyrosine-p
330	83	2.1	4162	2	T42633	connectin/titin -
331	83	2.1	5175	2	T20992	hypothetical prote
332	83	2.1	5198	2	T43290	hemocytin precurs
333	83	2.1	10223	2	T30225	polyketide synthas
334	82.5	2.0	376	1	RDEC2R	ribonucleoside-dip
335	82.5	2.0	376	2	H85862	ribonucleoside-dip
336	82.5	2.0	376	2	F91018	ribonucleoside-dip
337	82.5	2.0	385	1	S29844	transforming prote
338	82.5	2.0	424	2	T25774	hypothetical prote
339	82.5	2.0	428	2	S03767	cellulase (EC 3.2.
340	82.5	2.0	494	2	A43934	isocitrate dehydro
341	82.5	2.0	560	2	AD2389	serine/threonine k
342	82.5	2.0	669	2	S65551	factor H - bovine
343	82.5	2.0	702	1	SHECGD	guanosine-3',5'-bi
344	82.5	2.0	702	2	E91194	(p)ppGpp synthetas
345	82.5	2.0	702	2	F86041	guanosine-3',5'-bi
346	82.5	2.0	746	2	S52770	subtilisin-like pr
347	82.5	2.0	757	2	JC7519	subtilisin-like se
348	82.5	2.0	899	2	T11578	probable lipooxygen
349	82.5	2.0	941	2	D82599	hypothetical prote
350	82.5	2.0	941	2	A82797	hypothetical prote
351	82.5	2.0	974	1	URHUAP	peptidylglycine mo
352	82.5	2.0	1204	2	S35475	pol polyprotein -
353	82.5	2.0	1383	2	T13052	guanine nucleotide
354	82.5	2.0	1747	2	A45974	collagen alpha 1(X
355	82.5	2.0	2109	1	ZLVN	genome polyprotein

356	82.5	2.0	3381	2	T42389	versican precursor
357	82	2.0	161	2	T35350	hypothetical prote
358	82	2.0	196	2	A71325	hypothetical prote
359	82	2.0	372	1	OPJGBP	lignin peroxidase
360	82	2.0	417	1	S22784	acetyl-CoA C-acylt
361	82	2.0	467	2	T34874	hypothetical prote
362	82	2.0	518	2	D64576	hypothetical prote
363	82	2.0	551	2	E72234	conserved hypothet
364	82	2.0	581	2	A42743	pol polyprotein -
365	82	2.0	610	2	T41399	probable cyclophil
366	82	2.0	616	2	T32753	hypothetical prote
367	82	2.0	741	2	B54908	phospholipase A2 c
368	82	2.0	881	1	I48697	protein-tyrosine k
369	82	2.0	1085	2	T03531	cobN protein homol
370	82	2.0	1196	1	GNMVG	HIV-1 retropepsin
371	82	2.0	1196	1	GNMVRV	HIV-1 retropepsin
372	82	2.0	1244	2	S29083	guanine-nucleotide
373	82	2.0	1355	2	T00075	hypothetical prote
374	82	2.0	1377	2	T19214	UDP-glucose-glycop
375	82	2.0	1875	2	A36429	integrin beta-4 ch
376	82	2.0	3054	1	GNBVEV	genome polyprotein
377	82	2.0	3131	2	S39842	enniatin synthetas
378	82	2.0	3707	2	S18252	heparan sulfate pr
379	82	2.0	6420	2	T30283	polyketide synthas
380	81.5	2.0	236	2	C70577	hypothetical prote
381	81.5	2.0	284	2	C72757	probable phosphate
382	81.5	2.0	373	2	S48228	3-isopropylmalate
383	81.5	2.0	432	2	A90465	hypothetical prote
384	81.5	2.0	435	2	E96784	hypothetical prote
385	81.5	2.0	465	2	B81658	2-oxo acid dehydro
386	81.5	2.0	482	2	D75346	glutamyl-tRNA(Gln)
387	81.5	2.0	508	2	S44950	lmbC protein - Str
388	81.5	2.0	593	2	S45281	coagulation factor
389	81.5	2.0	599	2	G87322	methyl-accepting c
390	81.5	2.0	623	2	B82536	ABC transporter AT
391	81.5	2.0	627	2	G86156	T14P4.5 protein -
392	81.5	2.0	630	2	T48369	hypothetical prote
393	81.5	2.0	663	2	S64824	hypothetical prote
394	81.5	2.0	748	2	T37097	probable secreted
395	81.5	2.0	797	2	C85164	hypothetical prote
396	81.5	2.0	797	2	H71412	hypothetical prote
397	81.5	2.0	833	2	E82708	ATP-dependent heli
398	81.5	2.0	1096	1	S61917	protein kinase C (
399	81.5	2.0	1203	2	S26650	DNA-binding protei
400	81.5	2.0	1339	2	G84764	hypothetical prote
401	81.5	2.0	1964	2	T09059	notch4 - mouse
402	81.5	2.0	2033	2	T30849	actin binding prot
403	81.5	2.0	2207	2	S09553	genome polyprotein
404	81	2.0	232	2	B70653	hypothetical prote
405	81	2.0	261	2	T36705	probable rRNA meth
406	81	2.0	329	2	AG0519	probable aldo/keto
407	81	2.0	339	1	KHHUB	cathepsin B (EC 3.
408	81	2.0	359	2	S59392	probable membrane
409	81	2.0	360	2	I40347	recombination prot
410	81	2.0	407	2	H69064	serine/threonine p
411	81	2.0	441	2	F86277	F14L17.10 protein
412	81	2.0	447	2	G87320	hypothetical prote

413	81	2.0	454	2	T50193	probable seryl-trn
414	81	2.0	514	2	S49036	threonine synthase
415	81	2.0	514	2	T39213	threonine synthase
416	81	2.0	550	2	E90723	probable fumarate
417	81	2.0	550	2	E85574	probable fumarate
418	81	2.0	554	2	T06374	probable pectinest
419	81	2.0	554	2	T06468	pectinesterase (EC
420	81	2.0	594	2	AI0673	probable hydrolase
421	81	2.0	608	2	I53269	prolactin receptor
422	81	2.0	682	2	B86336	hypothetical prote
423	81	2.0	725	2	T20674	hypothetical prote
424	81	2.0	740	2	E69420	hydrogenase expres
425	81	2.0	763	2	C86733	penicillin-binding
426	81	2.0	770	2	F65028	Penicillin-binding
427	81	2.0	827	2	S29955	surface glycoprote
428	81	2.0	934	2	C81298	probable formate d
429	81	2.0	963	2	T09478	ubiquitin thiolest
430	81	2.0	977	2	S14183	DNA-directed RNA p
431	81	2.0	979	2	A39792	transcription acti
432	81	2.0	996	2	T47518	serine/threonine p
433	81	2.0	1006	2	T13331	probable tail prot
434	81	2.0	1051	2	AI2216	hypothetical prote
435	81	2.0	1070	2	T00767	hypothetical prote
436	81	2.0	1173	2	T52575	gigantea protein [
437	81	2.0	1313	1	VGUVPT	M polyprotein - Pu
438	81	2.0	2288	2	S41080	calcium channel al
439	81	2.0	2607	2	T31678	bacitracin synthet
440	81	2.0	3869	2	A48205	All-1 protein +GTE
441	81	2.0	4092	1	S38128	dynein heavy chain
442	81	2.0	4302	2	A38971	polycystic kidney
443	80.5	2.0	304	2	B83397	pyrroloquinoline q
444	80.5	2.0	376	2	AD0791	ribonucleoside-dip
445	80.5	2.0	412	1	S75358	coproporphyrinogen
446	80.5	2.0	413	2	JC2520	beta-fructofuranos
447	80.5	2.0	421	2	T51055	hypothetical prote
448	80.5	2.0	513	2	G96757	probable protein A
449	80.5	2.0	513	2	H69735	endo-1,4-beta-xyla
450	80.5	2.0	579	2	T30635	hypothetical prote
451	80.5	2.0	592	2	S25705	Ig mu chain - shee
452	80.5	2.0	662	2	T17211	hypothetical prote
453	80.5	2.0	692	2	T28783	hypothetical prote
454	80.5	2.0	741	2	A83271	hypothetical prote
455	80.5	2.0	755	2	T00066	hypothetical prote
456	80.5	2.0	978	2	T00336	hypothetical prote
457	80.5	2.0	988	2	T03307	hypothetical 109.6
458	80.5	2.0	1205	1	A38943	nitric-oxide synth
459	80.5	2.0	1322	2	H86196	hypothetical prote
460	80.5	2.0	1571	2	T13711	polyprotein - frui
461	80.5	2.0	1621	2	T30200	protein-tyrosine k
462	80.5	2.0	8563	2	T30226	polyketide synthas
463	80	2.0	302	1	S31818	myb-related protei
464	80	2.0	335	2	JH0813	GTP-binding regula
465	80	2.0	337	2	AH2719	delta-aminolevulin
466	80	2.0	342	2	S18728	recombination prot
467	80	2.0	350	2	T00892	hypothetical prote
468	80	2.0	360	2	D97501	porphobilinogen sy
469	80	2.0	370	2	T15095	hypothetical prote

470	80	2.0	377	1	RGMSA1	GTP-binding regula
471	80	2.0	380	1	RGHUA1	GTP-binding regula
472	80	2.0	394	1	RGHYAE	GTP-binding regula
473	80	2.0	394	1	RGMSA2	GTP-binding regula
474	80	2.0	394	1	RGBOGA	GTP-binding regula
475	80	2.0	394	1	RGHYA2	GTP-binding regula
476	80	2.0	394	1	RGRTA2	GTP-binding regula
477	80	2.0	394	2	S33458	GTP-binding regula
478	80	2.0	395	1	RGHUA2	GTP-binding regula
479	80	2.0	400	1	ZBBEI4	44.1K zinc-binding
480	80	2.0	404	2	AI3538	phosphopantothenoy
481	80	2.0	411	2	S58105	Cu metalloregulato
482	80	2.0	419	2	S34421	GTP-binding regula
483	80	2.0	507	2	B42360	cellulase (EC 3.2.
484	80	2.0	534	2	G88924	protein R02C2.1 [i
485	80	2.0	656	1	XJSOKP	transketolase (EC
486	80	2.0	665	1	P2BPF6	P2 protein - phage
487	80	2.0	842	1	JDVLVS	DNA-directed DNA p
488	80	2.0	846	2	S52418	GTP-binding regula
489	80	2.0	855	1	JQ2004	env polyprotein -
490	80	2.0	884	2	E89010	protein R08F11.1 [
491	80	2.0	890	2	A85501	protein PII-uridyl
492	80	2.0	890	2	A90650	protein PII-uridyl
493	80	2.0	899	1	GNMVM	pol polyprotein -
494	80	2.0	930	2	T20817	hypothetical prote
495	80	2.0	935	2	T16489	hypothetical prote
496	80	2.0	1014	2	JE0333	klotho protein - r
497	80	2.0	1016	1	A46079	protein kinase C (
498	80	2.0	1029	2	F87369	TonB-dependent rec
499	80	2.0	1047	2	S19508	MSH3 protein - yea
500	80	2.0	1068	2	T48756	mitochondrial nico
501	80	2.0	1206	2	T30555	nitric-oxide synth
502	80	2.0	1206	2	E87072	hypothetical prote
503	80	2.0	1317	2	A54831	nuclear pore compl
504	80	2.0	1354	2	T48198	hypothetical prote
505	80	2.0	1390	1	TVHUME	hepatocyte growth
506	80	2.0	1475	2	B33135	gtfB protein precu
507	80	2.0	2535	2	T02646	hypothetical prote
508	80	2.0	3005	2	T08841	polyprotein - dour
509	80	2.0	4543	1	A53102	alpha-2-macroglobu
510	80	2.0	4544	1	S02392	alpha-2-macroglobu
511	79.5	2.0	205	1	A26106	metalloproteinase
512	79.5	2.0	313	2	G02020	p37NB - human
513	79.5	2.0	322	1	A39350	3alpha-hydroxyster
514	79.5	2.0	428	2	S75037	folyl-polyglutamat
515	79.5	2.0	466	1	UFGP	fumarate hydratase
516	79.5	2.0	534	1	P1WL41	L1 protein - human
517	79.5	2.0	547	2	C82655	hypothetical prote
518	79.5	2.0	551	2	H69371	probable acid-CoA
519	79.5	2.0	556	1	A55483	transcription init
520	79.5	2.0	575	2	F69432	fumarate reductase
521	79.5	2.0	582	2	T00689	hypothetical prote
522	79.5	2.0	583	2	I39428	alcam - human
523	79.5	2.0	601	2	E95863	alcohol dehydrogen
524	79.5	2.0	633	2	T40124	kinesin-like motor
525	79.5	2.0	647	2	T51808	probable auxin eff
526	79.5	2.0	657	2	AE0431	probable exported

527	79.5	2.0	696	2	E71510	probable oligopept
528	79.5	2.0	703	2	T43557	F-box/WD-repeat pr
529	79.5	2.0	723	2	AC1241	polynucleotide pho
530	79.5	2.0	819	2	I48859	tyro 10 receptor k
531	79.5	2.0	856	1	VCLJFP	env polyprotein pr
532	79.5	2.0	891	2	H83218	heme acquisition p
533	79.5	2.0	912	1	RDBHNS	nitrate reductase
534	79.5	2.0	914	2	T07065	probable lipoxigen
535	79.5	2.0	915	1	RDBHNS	nitrate reductase
536	79.5	2.0	944	2	H64650	translation initia
537	79.5	2.0	965	2	T38430	hypothetical prote
538	79.5	2.0	1161	2	S18738	pol protein - simi
539	79.5	2.0	1172	2	AD2310	hypothetical prote
540	79.5	2.0	1211	2	T08540	hypothetical prote
541	79.5	2.0	1299	1	S06119	membrane protein p
542	79.5	2.0	1314	2	G02870	KIAA0197 protein -
543	79.5	2.0	1422	2	T18363	DNA-directed RNA p
544	79.5	2.0	1687	2	T30176	EGF repeat transme
545	79.5	2.0	2154	2	F83068	hypothetical prote
546	79.5	2.0	2541	2	S11661	talin - mouse
547	79.5	2.0	3172	2	S22012	erythronolide synt
548	79	2.0	266	2	S02510	nifM protein - Kle
549	79	2.0	310	2	S65966	succinate-CoA liga
550	79	2.0	332	2	I48691	regulatory protein
551	79	2.0	352	2	T33433	hypothetical prote
552	79	2.0	370	2	F86338	protein F2D10.2 [i
553	79	2.0	372	2	B32322	lignin peroxidase
554	79	2.0	396	1	XNECD	aspartate transami
555	79	2.0	396	2	A85619	aspartate aminotra
556	79	2.0	396	2	C90755	aspartate aminotra
557	79	2.0	441	2	C85761	anthranilate synth
558	79	2.0	454	2	AI1606	acetyl-CoA carboxy
559	79	2.0	468	2	T22397	hypothetical prote
560	79	2.0	513	2	S63701	mannosyl-oligosacc
561	79	2.0	520	1	NNEC1	anthranilate synth
562	79	2.0	520	2	D90858	anthranilate synth
563	79	2.0	552	2	A96756	hypothetical prote
564	79	2.0	555	2	AE2208	hypothetical prote
565	79	2.0	583	2	JC6504	alpha,alpha-trehal
566	79	2.0	590	2	E87337	ferrous iron trans
567	79	2.0	599	2	AG0858	sulfite reductase
568	79	2.0	601	2	H81282	probable translati
569	79	2.0	633	2	S47144	mating type A prot
570	79	2.0	638	2	H82690	hypothetical prote
571	79	2.0	657	2	H70872	probable ctpD prot
572	79	2.0	704	2	T19942	hypothetical prote
573	79	2.0	711	2	S66261	X-Pro dipeptidyl-p
574	79	2.0	755	2	T19945	hypothetical prote
575	79	2.0	764	2	T05768	subtilisin-like pr
576	79	2.0	773	2	T46188	inhibition protein
577	79	2.0	787	2	A81940	probable phenylala
578	79	2.0	798	2	JC7500	qik protein - chic
579	79	2.0	800	2	A84293	helicase [imported
580	79	2.0	804	2	A96494	protein F7F22.16 [
581	79	2.0	843	1	JDVLJ1	DNA-directed DNA p
582	79	2.0	890	2	G64740	[protein-PII] urid
583	79	2.0	1023	2	E71376	conserved hypothet

584	79	2.0	1043	2	H83071	RND multidrug effl
585	79	2.0	1091	2	T48444	hypothetical prote
586	79	2.0	1142	2	T46155	hypothetical prote
587	79	2.0	1161	2	G81186	conserved hypothet
588	79	2.0	1200	2	E84473	probable retroelem
589	79	2.0	1350	2	G89756	protein T23E7.1 [i
590	79	2.0	1400	2	B70963	hypothetical prote
591	79	2.0	1422	2	T42636	protein-tyrosine-p
592	79	2.0	1506	2	S52957	bimD protein - Eme
593	79	2.0	1520	2	T00273	hypothetical prote
594	79	2.0	1558	2	AB2457	two-component hybr
595	79	2.0	2240	2	T37057	probable multi-dom
596	79	2.0	2508	2	S61441	surface-associated
597	78.5	1.9	189	2	T46088	proline-rich prote
598	78.5	1.9	282	1	JC4041	D-arabinitol 2-deh
599	78.5	1.9	284	2	G87313	conserved hypothet
600	78.5	1.9	304	2	T51822	1-(5-phosphoribosy
601	78.5	1.9	332	2	F87319	conserved hypothet
602	78.5	1.9	352	2	I77374	pregnancy-specific
603	78.5	1.9	373	1	S48225	3-isopropylmalate
604	78.5	1.9	376	2	AH0148	ribonucleoside-dip
605	78.5	1.9	413	2	S47527	extracellular sucra
606	78.5	1.9	414	2	T39403	probable mannose-1
607	78.5	1.9	476	2	S09152	translation elonga
608	78.5	1.9	482	2	G75483	probable leucyl am
609	78.5	1.9	494	2	JX0065	anthranilate synth
610	78.5	1.9	495	1	A26396	T-cell surface gly
611	78.5	1.9	505	2	T39645	folypolyglutamate
612	78.5	1.9	513	2	T37806	probable flavoprot
613	78.5	1.9	519	1	S75850	pet112 protein - S
614	78.5	1.9	545	2	T02005	protoporphyrinogen
615	78.5	1.9	552	2	E87226	conserved membrane
616	78.5	1.9	555	2	A33723	Cypridina-luciferi
617	78.5	1.9	563	2	AH2187	DNA mismatch repai
618	78.5	1.9	566	1	T43706	isobutyryl-CoA mut
619	78.5	1.9	571	2	S49119	embryonic/neonatal
620	78.5	1.9	582	2	S29314	phytoene dehydroge
621	78.5	1.9	592	2	B81009	BirA protein/Bvg a
622	78.5	1.9	592	2	H82031	probable biotin-[a
623	78.5	1.9	599	1	A34231	sulfite reductase
624	78.5	1.9	646	2	T02643	hypothetical prote
625	78.5	1.9	715	2	B84670	probable phosphopr
626	78.5	1.9	827	2	JC4900	transferred entry
627	78.5	1.9	848	1	JC1351	transforming growt
628	78.5	1.9	855	2	S42621	protein-tyrosine k
629	78.5	1.9	859	2	T06429	lipxygenase (EC 1
630	78.5	1.9	896	2	I56563	interleukin-3 rece
631	78.5	1.9	988	1	S35362	protein kinase C (
632	78.5	1.9	1051	2	A39712	kinase-like protei
633	78.5	1.9	1146	2	A55532	myosin-heavy-chain
634	78.5	1.9	1174	2	AE2911	pyruvate carboxyla
635	78.5	1.9	1174	2	C97686	pyruvate carboxyla
636	78.5	1.9	1288	2	T42756	5-oxoprolinase (AT
637	78.5	1.9	1317	2	B83346	probable non-ribos
638	78.5	1.9	1461	2	B70588	probable polyketid
639	78.5	1.9	1615	2	JE0372	low density lipopr
640	78.5	1.9	1742	2	S24600	projectin - fruit

641	78.5	1.9	1815	2	S73021	polyketide synthas
642	78.5	1.9	1822	2	F87203	polyketide synthas
643	78.5	1.9	2035	2	A40718	host cell factor C
644	78.5	1.9	2183	2	T37218	hypothetical prote
645	78.5	1.9	2629	2	T32735	telomerase-associa
646	78.5	1.9	3345	2	T13423	hypothetical prote
647	78.5	1.9	3390	1	GNWVD3	genome polyprotein
648	78.5	1.9	7576	2	T17428	FK506 polyketide s
649	78	1.9	215	2	E97090	deoxyribose-phosph
650	78	1.9	277	2	F84336	hypothetical prote
651	78	1.9	286	2	F95389	protein [imported
652	78	1.9	347	2	T20103	hypothetical prote
653	78	1.9	371	2	AH0686	hypothetical prote
654	78	1.9	398	2	H86424	unknown protein [i
655	78	1.9	400	2	JC5358	two-component sens
656	78	1.9	426	2	H69127	histidinol dehydro
657	78	1.9	443	2	T06809	protein kinase hom
658	78	1.9	444	2	T01721	hypothetical prote
659	78	1.9	451	2	T00694	hypothetical prote
660	78	1.9	470	2	B24670	probable a factor
661	78	1.9	494	2	D70579	probable murC prot
662	78	1.9	508	2	C70908	hypothetical prote
663	78	1.9	586	2	PC6006	scaffolding protei
664	78	1.9	590	2	S37157	NADPH-ferrihemopro
665	78	1.9	669	2	B96036	probable aldehyde
666	78	1.9	684	2	E64496	ATP-dependent RNA
667	78	1.9	708	2	F75576	probable oxidoredu
668	78	1.9	732	1	S05238	peptidyl-dipeptida
669	78	1.9	832	2	JH0393	fibroblast growth
670	78	1.9	832	2	S71785	DNA-directed DNA p
671	78	1.9	843	1	JDVLVR	DNA-directed DNA p
672	78	1.9	860	2	T22974	hypothetical prote
673	78	1.9	871	2	G86586	DNA topoisomerase
674	78	1.9	871	2	D72038	DNA topoisomerase
675	78	1.9	898	2	S47489	receptor tyrosine
676	78	1.9	900	2	S47029	nitrate reductase
677	78	1.9	942	2	T20287	hypothetical prote
678	78	1.9	970	2	C84488	hypothetical prote
679	78	1.9	997	2	A87320	TonB-dependent rec
680	78	1.9	1286	1	RJBOP	interphotoreceptor
681	78	1.9	1300	2	A36502	insulin receptor-r
682	78	1.9	1306	1	A31759	peptidyl-dipeptida
683	78	1.9	1322	2	B71440	hypothetical prote
684	78	1.9	1456	2	T01397	LTR gag/pol polyp
685	78	1.9	1601	2	AE2011	hypothetical prote
686	78	1.9	2348	2	AD1841	hypothetical prote
687	78	1.9	2477	2	S14428	fibronectin precur
688	77.5	1.9	237	2	B82986	hypothetical prote
689	77.5	1.9	267	2	B87625	hypothetical prote
690	77.5	1.9	301	2	G69519	hypothetical prote
691	77.5	1.9	310	2	S20889	superantigen Mtv1
692	77.5	1.9	315	2	JH0554	superantigen Mtv13
693	77.5	1.9	315	2	JH0551	superantigen Mtv1/
694	77.5	1.9	316	2	C82561	drug tolerance pro
695	77.5	1.9	325	2	T25122	hypothetical prote
696	77.5	1.9	395	2	A95860	hypothetical prote
697	77.5	1.9	395	2	T45599	hypothetical prote

698	77.5	1.9	412	2	T35514	probable glycosyl
699	77.5	1.9	425	2	A95242	hypothetical prote
700	77.5	1.9	460	2	G01210	guanine nucleotide
701	77.5	1.9	466	2	JC5897	killer cell inhibi
702	77.5	1.9	477	2	F86670	lysine specific pe
703	77.5	1.9	487	2	A82835	anthranilate synth
704	77.5	1.9	496	2	D75261	conserved hypothet
705	77.5	1.9	517	2	T06274	probable lipoxxygen
706	77.5	1.9	522	2	A46103	transmembrane glyc
707	77.5	1.9	575	2	T11753	mullerian inhibiti
708	77.5	1.9	599	2	T18316	hypothetical prote
709	77.5	1.9	604	2	T36966	hypothetical prote
710	77.5	1.9	632	2	T45858	hypothetical prote
711	77.5	1.9	656	2	H82862	conjugal transfer
712	77.5	1.9	756	2	AB1452	chitinase B homolo
713	77.5	1.9	762	2	H83348	probable acylase P
714	77.5	1.9	775	2	S55345	protein-tyrosine-p
715	77.5	1.9	858	2	JC7683	taste receptor T1R
716	77.5	1.9	923	2	T08033	serine/threonine p
717	77.5	1.9	927	2	T08034	serine/threonine p
718	77.5	1.9	1041	2	E70760	probable ileS prot
719	77.5	1.9	1042	2	T46406	hypothetical prote
720	77.5	1.9	1057	2	A42109	glycine dehydrogen
721	77.5	1.9	1077	2	S45395	hypothetical prote
722	77.5	1.9	1285	1	BTQPD	dermonecrotic toxi
723	77.5	1.9	1299	2	I58401	protein-tyrosine k
724	77.5	1.9	1316	2	T50444	hypothetical UPF00
725	77.5	1.9	1434	2	T22202	hypothetical prote
726	77.5	1.9	1664	2	F84485	probable retroelem
727	77.5	1.9	1678	2	T35547	hypothetical prote
728	77.5	1.9	1769	2	S53378	probable membrane
729	77.5	1.9	1846	2	T10670	hypothetical prote
730	77.5	1.9	1940	1	S04090	myosin heavy chain
731	77.5	1.9	2118	2	S72705	mycocerosate synth
732	77.5	1.9	2207	1	GNNY5P	genome polyprotein
733	77.5	1.9	2491	1	A28372	insulin-like growt
734	77.5	1.9	2649	2	A40937	bullous pemphigoid
735	77.5	1.9	3016	2	S77300	hypothetical prote
736	77.5	1.9	4859	2	S74173	ryanodine receptor
737	77.5	1.9	5149	2	F83345	probable non-ribos
738	77	1.9	225	2	G75074	hypothetical prote
739	77	1.9	256	2	T17635	hypothetical prote
740	77	1.9	263	2	T28146	class II histocomp
741	77	1.9	309	2	T08150	chitinase (EC 3.2.
742	77	1.9	335	1	KHBOB	cathepsin B (EC 3.
743	77	1.9	344	2	JC5602	cAMP response elem
744	77	1.9	345	2	JQ0429	hypothetical 37.1K
745	77	1.9	354	2	A95368	probable CheB2 che
746	77	1.9	355	2	G83003	A / G specific ade
747	77	1.9	372	1	OPJG3P	lignin peroxidase
748	77	1.9	381	2	H75173	udp-n-acetylglucos
749	77	1.9	400	2	A69270	molybdenum cofacto
750	77	1.9	406	1	REHUK	renin (EC 3.4.23.1
751	77	1.9	417	2	A44194	poliovirus recepto
752	77	1.9	426	2	AI0287	conserved hypothet
753	77	1.9	457	2	T44879	acetyltransferase
754	77	1.9	458	1	YTBSY8	tetracycline resis

755	77	1.9	459	2	F64688	proteinase (EC 3.4
756	77	1.9	459	2	AC2308	hypothetical prote
757	77	1.9	474	2	B38634	tumor necrosis fac
758	77	1.9	486	2	A41537	DNA-binding protei
759	77	1.9	518	2	H81973	probable chromosom
760	77	1.9	554	2	AC0568	FdrA protein [impo
761	77	1.9	555	2	H84476	probable Athila re
762	77	1.9	569	2	C69422	hydrogenase (EC 1:
763	77	1.9	569	2	C91195	hypothetical prote
764	77	1.9	569	2	D86042	hypothetical prote
765	77	1.9	569	2	A65167	hypothetical 62.3K
766	77	1.9	605	2	T07123	nine-cis-epoxycaro
767	77	1.9	663	2	S69548	zeaxanthin epoxida
768	77	1.9	732	2	A83481	probable TonB-depe
769	77	1.9	736	1	S31809	translation elonga
770	77	1.9	794	2	I58376	hypothetical prote
771	77	1.9	832	1	JDVLA1	DNA-directed DNA p
772	77	1.9	832	1	JDVLVB	DNA-directed DNA p
773	77	1.9	836	2	C82726	DNA uptake protein
774	77	1.9	843	2	S35527	DNA-directed DNA p
775	77	1.9	884	2	S66308	nitrate reductase
776	77	1.9	886	2	S48371	hypothetical prote
777	77	1.9	972	1	URBOAP	peptidylglycine mo
778	77	1.9	980	2	AH1844	hypothetical prote
779	77	1.9	1075	2	D70568	hypothetical prote
780	77	1.9	1202	2	S71424	nitric-oxide synth
781	77	1.9	1216	2	H85023	hypothetical prote
782	77	1.9	1306	2	S25370	MSB2 protein - yea
783	77	1.9	1440	2	JC6312	protein-tyrosine-p
784	77	1.9	1504	2	T17426	FK506 polyketide s
785	77	1.9	1736	2	T05174	hypothetical prote
786	77	1.9	2025	2	D86201	protein F12K11.6 [
787	77	1.9	2137	1	SJHUB	spectrin beta chai
788	77	1.9	2142	1	ZLVNPV	genome polyprotein
789	77	1.9	2223	2	A47447	calcium channel pr
790	77	1.9	4836	2	T14346	herc2 protein - mo
791	77	1.9	4868	2	B54161	ryanodine-binding
792	77	1.9	4924	2	T50176	probable peptide s
793	76.5	1.9	108	2	D86826	hypothetical prote
794	76.5	1.9	225	2	T34201	hypothetical prote
795	76.5	1.9	252	2	S33323	nonspecific cross-
796	76.5	1.9	266	2	G81706	conserved hypothet
797	76.5	1.9	346	2	G83127	conserved hypothet
798	76.5	1.9	351	2	D90264	biotin synthase (b
799	76.5	1.9	366	2	E72355	hypothetical prote
800	76.5	1.9	410	2	H97639	probable D-amino a
801	76.5	1.9	414	2	B96808	protein F28K19.2 [
802	76.5	1.9	445	2	F83881	hypothetical prote
803	76.5	1.9	504	2	S28298	hypothetical prote
804	76.5	1.9	522	2	T28113	hypothetical prote
805	76.5	1.9	534	2	A82278	citrate lyase, alp
806	76.5	1.9	540	2	D69274	medium-chain acyl-
807	76.5	1.9	565	2	T47423	hypothetical prote
808	76.5	1.9	569	2	C69471	probable fatty-aci
809	76.5	1.9	580	2	T30583	probable peptide s
810	76.5	1.9	591	2	I52728	reduced folate car
811	76.5	1.9	603	2	JC7900	beta-N-acetylgluco

812	76.5	1.9	616	2	T32131	hypothetical prote
813	76.5	1.9	632	2	T00679	hypothetical prote
814	76.5	1.9	635	2	A45266	MPL-P protein prec
815	76.5	1.9	746	2	E83250	still frameshift 3
816	76.5	1.9	750	2	AH3158	hypothetical prote
817	76.5	1.9	816	2	S46268	ataxin-1 - human
818	76.5	1.9	832	2	F98128	insertion element
819	76.5	1.9	855	2	B83193	DNA mismatch repai
820	76.5	1.9	893	2	S51603	receptor-like tyro
821	76.5	1.9	925	2	T37475	lipoprotein recept
822	76.5	1.9	963	2	T40290	hypothetical prote
823	76.5	1.9	991	2	I78843	receptor protein-t
824	76.5	1.9	998	2	H75005	ATP-dependent prot
825	76.5	1.9	1039	2	G83748	alpha-mannosidase
826	76.5	1.9	1047	2	T34946	probable isoleucyl
827	76.5	1.9	1049	2	T30525	alpha-mannosidase
828	76.5	1.9	1147	1	S47647	nitric-oxide synth
829	76.5	1.9	1218	2	A88429	protein C28A5.2 [i
830	76.5	1.9	1238	1	A40185	virulence protein
831	76.5	1.9	1386	2	T00257	hypothetical prote
832	76.5	1.9	1390	2	A45455	nucleoporin 155 -
833	76.5	1.9	1492	2	T18560	DNA-directed DNA p
834	76.5	1.9	1577	2	T15851	hypothetical prote
835	76.5	1.9	1645	2	T31339	carbamoyl-phosphat
836	76.5	1.9	1696	2	T27447	hypothetical prote
837	76.5	1.9	1857	2	S31212	collagen alpha 1(X
838	76.5	1.9	1888	2	S78476	collagen alpha 1(X
839	76.5	1.9	2109	2	I38414	transcription fact
840	76.5	1.9	2188	2	A70984	probable polyketid
841	76.5	1.9	2201	2	AH0095	probable sideropho
842	76.5	1.9	2346	2	I38928	acetyl-CoA carboxy
843	76.5	1.9	2383	2	D64962	probable membrane
844	76.5	1.9	2531	2	T31070	notch homolog - se
845	76.5	1.9	2535	2	AC0304	probable hemolysin
846	76.5	1.9	3396	1	A42551	genome polyprotein
847	76.5	1.9	5147	1	IJFFTM	cadherin-related t
848	76.5	1.9	6831	2	A88852	protein unc-22 [im
849	76.5	1.9	6839	2	S57242	twitchin [similar
850	76.5	1.9	7160	2	T27935	hypothetical prote
851	76	1.9	217	2	T05820	hypothetical prote
852	76	1.9	224	2	AH0168	hypothetical prote
853	76	1.9	265	2	A48304	cytochrome-c oxida
854	76	1.9	286	2	AH2416	hypothetical prote
855	76	1.9	288	2	T30648	probable DNA-bindi
856	76	1.9	294	2	A48844	TGF alpha-like pro
857	76	1.9	319	2	AE1443	gp47 (Bacteriophag
858	76	1.9	319	2	AI1733	gp47 (Bacteriophag
859	76	1.9	324	2	H82681	integrase/recombin
860	76	1.9	358	2	T25010	hypothetical prote
861	76	1.9	359	2	F90055	conserved hypothet
862	76	1.9	367	2	C96537	hypothetical prote
863	76	1.9	367	2	T02000	hypothetical prote
864	76	1.9	405	2	A60534	P2B/LAMP-1 precurs
865	76	1.9	423	2	E72004	adenosylmethionine
866	76	1.9	423	2	F86620	hypothetical prote
867	76	1.9	466	2	T36212	replication initia
868	76	1.9	468	1	UFHUM	fumarate hydratase

869	76	1.9	475	2	S20250	splicing factor U2
870	76	1.9	476	2	A39406	dihydrolipoamide d
871	76	1.9	477	2	C95945	conserved hypothet
872	76	1.9	490	2	T37884	transcription fact
873	76	1.9	496	2	B71489	probable exodeoxyr
874	76	1.9	513	2	S54469	hypothetical prote
875	76	1.9	518	2	F81027	chromosomal replic
876	76	1.9	565	2	B72660	probable type II D
877	76	1.9	585	2	AI2786	arginyl-tRNA synth
878	76	1.9	585	2	C97566	arginyl-tRNA synth
879	76	1.9	593	2	F75032	rnase l inhibitor
880	76	1.9	595	2	T49384	related to NRD1 pr
881	76	1.9	611	2	E72114	oligoendopeptidase
882	76	1.9	611	2	H86507	oligopeptidase [im
883	76	1.9	612	2	G69797	conserved hypothet
884	76	1.9	622	2	E81793	probable inner mem
885	76	1.9	623	2	T07664	lipoxygenase (EC 1
886	76	1.9	626	2	A42094	regulator protein
887	76	1.9	638	2	S46499	NADP-dependent mal
888	76	1.9	646	1	WZBEC8	68.6K capsid prote
889	76	1.9	655	2	C75323	conserved hypothet
890	76	1.9	662	2	I37892	IL12 receptor comp
891	76	1.9	728	1	A38084	galactose oxidase
892	76	1.9	728	2	C85072	hypothetical prote
893	76	1.9	734	2	T07280	photosystem I P700
894	76	1.9	789	2	I52701	K-cadherin - rat
895	76	1.9	809	2	S67665	ubiquitin-specific
896	76	1.9	830	2	A30359	P-selectin precurs
897	76	1.9	852	1	GNLJGA	pol polyprotein -
898	76	1.9	862	2	S22153	lipoxygenase (EC 1
899	76	1.9	960	2	G84652	probable receptor-
900	76	1.9	981	2	S51604	receptor-like tyro
901	76	1.9	991	2	E83137	probable nonriboso
902	76	1.9	1000	2	T13636	probable minor str
903	76	1.9	1005	2	S49015	receptor tyrosine
904	76	1.9	1015	2	S68141	nuclear protein HI
905	76	1.9	1016	2	AC2900	oxoglutarate dehyd
906	76	1.9	1016	2	D97675	2-oxoglutarate deh
907	76	1.9	1045	2	G69167	cobalamin biosynth
908	76	1.9	1089	2	E82987	hypothetical prote
909	76	1.9	1095	2	T13964	probable histone d
910	76	1.9	1114	2	B86423	hypothetical prote
911	76	1.9	1156	2	C87371	TonB-dependent rec
912	76	1.9	1187	1	JC4155	protein-tyrosine-p
913	76	1.9	1194	2	S70415	DNA-directed RNA p
914	76	1.9	1442	2	C82898	DNA polymerase III
915	76	1.9	1518	2	T28880	hypothetical prote
916	76	1.9	1596	2	A35927	190K DNA-binding p
917	76	1.9	1610	2	T11681	hypothetical prote
918	76	1.9	1646	1	WMTMS2	186K protein - cuc
919	76	1.9	2109	2	T17490	polyketide synthas
920	76	1.9	2318	2	S45306	notch 3 protein -
921	76	1.9	2386	1	FNHU	fibronectin precur
922	76	1.9	2554	1	TVFF7L	kinase-related pro
923	76	1.9	26926	1	I38344	titin, cardiac mus
924	75.5	1.9	293	2	AD2948	hypothetical prote
925	75.5	1.9	301	2	S75855	hypothetical prote

926	75.5	1.9	305	2	AC1513	oxidoreductase hom
927	75.5	1.9	322	2	G82018	lipopolysaccharide
928	75.5	1.9	324	2	A84295	probable DNA helic
929	75.5	1.9	329	2	F98334	SN-glycerol 3-phos
930	75.5	1.9	332	2	AB2133	hypothetical prote
931	75.5	1.9	339	2	T31859	hypothetical prote
932	75.5	1.9	341	2	S26686	cAMP response elem
933	75.5	1.9	346	2	A82971	low specificity l-
934	75.5	1.9	358	2	C84713	probable dioxygena
935	75.5	1.9	376	2	B84360	citrate synthase {
936	75.5	1.9	393	2	S27881	beta-alanine synth
937	75.5	1.9	395	2	T24578	hypothetical prote
938	75.5	1.9	403	2	B71378	probable recF prot
939	75.5	1.9	424	2	A34595	pregnancy-specific
940	75.5	1.9	426	1	T49035	acid phosphatase (
941	75.5	1.9	434	2	A75450	conserved hypothet
942	75.5	1.9	458	2	S12444	hypothetical prote
943	75.5	1.9	485	2	AE2165	hypothetical prote
944	75.5	1.9	499	2	G75600	cleavage and polya
945	75.5	1.9	503	2	E70853	probable acid-CoA
946	75.5	1.9	512	1	A39719	protein-tyrosine k
947	75.5	1.9	518	2	AD1731	hypothetical prote
948	75.5	1.9	532	2	JC5412	epidermal growth f
949	75.5	1.9	543	2	A53310	pheromone cAD1 bin
950	75.5	1.9	553	2	F75407	probable transport
951	75.5	1.9	568	2	JC5629	mullerian-inhibiti
952	75.5	1.9	570	2	A39597	phytoene dehydroge
953	75.5	1.9	601	2	JE0238	stress protein p66
954	75.5	1.9	625	2	C86955	hypothetical prote
955	75.5	1.9	625	2	S72993	glutamine-fructose
956	75.5	1.9	635	2	S19011	endo-1,4-beta-xyla
957	75.5	1.9	640	1	QYCHGM	phosphoenolpyruvat
958	75.5	1.9	641	2	B83653	nucleotidase precu
959	75.5	1.9	693	1	A41090	serine/threonine-s
960	75.5	1.9	704	2	I47228	carbonic anhydrase
961	75.5	1.9	711	2	G86526	hypothetical prote
962	75.5	1.9	711	2	A72098	hypothetical prote
963	75.5	1.9	773	1	QRRBG	secretory componen
964	75.5	1.9	789	2	A48337	genome polyprotein
965	75.5	1.9	801	2	PC6010	RNA helicase Gu -
966	75.5	1.9	832	1	JDVLVA	DNA-directed DNA p
967	75.5	1.9	871	1	I48696	protein-tyrosine k
968	75.5	1.9	908	2	T07409	lipoxxygenase (EC 1
969	75.5	1.9	910	2	D75524	alpha-dextran endo
970	75.5	1.9	917	1	RDMUNH	nitrate reductase
971	75.5	1.9	942	2	T19553	hypothetical prote
972	75.5	1.9	952	1	A32609	alpha-glucosidase
973	75.5	1.9	958	2	C86308	F20D23.9 protein -
974	75.5	1.9	989	2	S69711	hypothetical prote
975	75.5	1.9	1102	2	T12681	hypothetical prote
976	75.5	1.9	1111	2	T38407	leucyl-trna synthe
977	75.5	1.9	1116	2	T38073	serine/threonine-p
978	75.5	1.9	1206	2	T18557	probable hydrogena
979	75.5	1.9	1260	2	S28407	guanine nucleotide
980	75.5	1.9	1425	2	T31153	hypothetical prote
981	75.5	1.9	2222	2	T13924	sdk protein - frui
982	75.5	1.9	2628	2	T28651	hemagglutinin A -

983	75.5	1.9	3391	1	GNWVJA	genome polyprotein
984	75.5	1.9	3796	2	T18514	lysosomal traffick
985	75.5	1.9	6805	2	S20901	titin - rabbit (fr
986	75	1.9	242	2	F87687	nucleotidyltransfe
987	75	1.9	301	2	D82040	cysQ protein VC272
988	75	1.9	314	2	B75524	inosine-uridine pr
989	75	1.9	323	2	T02617	hypothetical prote
990	75	1.9	339	1	KHRTB	cathepsin B (EC 3.
991	75	1.9	345	2	E70484	recombination prot
992	75	1.9	346	2	D64680	conserved hypothet
993	75	1.9	362	2	S60614	growth promoting a
994	75	1.9	364	2	T45253	probable antiporte
995	75	1.9	378	2	AE3350	recA protein [impo
996	75	1.9	382	2	D84856	hypothetical prote
997	75	1.9	387	2	S60222	probable chlorophy
998	75	1.9	393	2	A45017	transcription fact
999	75	1.9	395	2	B96735	unknown protein F2
1000	75	1.9	410	2	AB0077	probable aminotran
1001	75	1.9	423	2	B86657	hypothetical prote
1002	75	1.9	440	2	S04168	streptokinase A pr
1003	75	1.9	447	2	S65686	protein phosphatas
1004	75	1.9	459	2	I48854	gene murine tumour
1005	75	1.9	459	2	D71827	carboxyl-terminal
1006	75	1.9	478	2	T02629	vacuolar processin
1007	75	1.9	492	2	S22646	splicing factor U2
1008	75	1.9	509	2	T05937	cytochrome P450 mo
1009	75	1.9	520	1	G86662	2',3'-cyclic-nucle
1010	75	1.9	534	2	S73037	probable phosphoma
1011	75	1.9	535	2	S19729	xylan 1,4-beta-xyl
1012	75	1.9	538	2	C86997	probable phospho-s
1013	75	1.9	645	2	T21574	hypothetical prote
1014	75	1.9	670	2	AI1847	two-component sens
1015	75	1.9	750	2	T42614	probable envelope
1016	75	1.9	752	2	G82798	hypothetical prote
1017	75	1.9	763	2	AG1460	alpha-glucosidase
1018	75	1.9	788	2	AG0786	secreted effector
1019	75	1.9	817	1	RRVGCT	RNA-directed RNA p
1020	75	1.9	828	2	G87584	hypothetical prote
1021	75	1.9	856	2	S23823	env polyprotein -
1022	75	1.9	857	2	S19886	env polyprotein E
1023	75	1.9	902	2	A55543	cmaA protein - Pse
1024	75	1.9	926	2	E96749	probable lipoxxygen
1025	75	1.9	945	2	A64714	helicase - Helicob
1026	75	1.9	952	2	S32954	hypothetical prote
1027	75	1.9	980	2	T05414	protein kinase hom
1028	75	1.9	995	2	H59432	RhoGAP protein hom
1029	75	1.9	1003	2	T13856	ksr protein - frui
1030	75	1.9	1025	2	A83186	probable RND efflu
1031	75	1.9	1032	2	D83637	serine/threonine p
1032	75	1.9	1036	2	A29832	HPI layer surface
1033	75	1.9	1044	1	DVBYE3	translation elonga
1034	75	1.9	1182	2	I48378	hairless protein -
1035	75	1.9	1365	2	T13991	nucleoporin 154 -
1036	75	1.9	1411	2	S40525	copper-transportin
1037	75	1.9	1450	2	A84780	probable ABC trans
1038	75	1.9	1457	1	A48066	protein-tyrosine-p
1039	75	1.9	1584	2	T18276	protein-tyrosine k

1040	75	1.9	1607	2	T02837	long chain fatty a
1041	75	1.9	1613	2	A43081	vitellogenin vit-2
1042	75	1.9	1620	2	S21045	complement protein
1043	75	1.9	1637	2	T00070	hypothetical prote
1044	75	1.9	1812	2	I49350	breast/ovarian can
1045	75	1.9	1940	1	A24922	myosin heavy chain
1046	75	1.9	2126	2	E70522	probable polyketid
1047	75	1.9	2684	2	A96521	protein F21D18.22
1048	75	1.9	3026	2	T28431	variant surface pr
1049	75	1.9	3491	2	T43231	probable 6-deoxyer
1050	74.5	1.8	207	2	I46964	metalloproteinase
1051	74.5	1.8	249	2	E87575	ABC transporter, A
1052	74.5	1.8	250	2	B64955	ABC-type transport
1053	74.5	1.8	250	2	H85808	hypothetical prote
1054	74.5	1.8	250	2	G90960	hypothetical prote
1055	74.5	1.8	250	2	AI0416	conserved hypothet
1056	74.5	1.8	288	2	T13644	lysin - Streptococ
1057	74.5	1.8	289	2	E90397	dihydrodipicolinat
1058	74.5	1.8	334	2	A75495	6-phosphofructokin
1059	74.5	1.8	339	2	B95932	probable sugar-pro
1060	74.5	1.8	341	2	S20827	cAMP response elem
1061	74.5	1.8	348	2	T40989	probable d-amino a
1062	74.5	1.8	350	2	D71514	probable sulfite r
1063	74.5	1.8	373	2	S48226	3-isopropylmalate
1064	74.5	1.8	376	2	A48060	erythroid Kruppel
1065	74.5	1.8	409	1	S72892	probable hexosyltr
1066	74.5	1.8	410	2	A70648	probable NADH2 deh
1067	74.5	1.8	412	2	S76639	probable transamin
1068	74.5	1.8	416	1	S33777	hepsin (EC 3.4.21.
1069	74.5	1.8	417	2	F90916	probable transport
1070	74.5	1.8	417	2	F64915	membrane protein y
1071	74.5	1.8	417	2	C85765	probable transport
1072	74.5	1.8	418	2	F83411	LasA proteinase pr
1073	74.5	1.8	428	2	H87214	probable glycosyl
1074	74.5	1.8	431	2	AE0795	isochorismate synt
1075	74.5	1.8	431	2	A45142	cleavage stimulati
1076	74.5	1.8	437	2	I57942	5-hydroxytryptamin
1077	74.5	1.8	450	1	S13730	pmbA protein - Esc
1078	74.5	1.8	450	2	D86121	maturation of anti
1079	74.5	1.8	450	2	D91280	maturation of anti
1080	74.5	1.8	467	2	A60667	cysteine proteinas
1081	74.5	1.8	475	2	AC0415	dihydrolipoamide d
1082	74.5	1.8	475	2	T39359	probable udp-n-ace
1083	74.5	1.8	518	2	JC7387	testis-abundant fi
1084	74.5	1.8	527	2	S32430	abrin-b precursor
1085	74.5	1.8	535	2	S78598	D-ribulokinase (EC
1086	74.5	1.8	537	2	G85021	protoporphyrinogen
1087	74.5	1.8	542	2	A28550	cyclohexanone mono
1088	74.5	1.8	554	2	AC0320	asparagine synthas
1089	74.5	1.8	566	2	A48860	beta-glucosidase,
1090	74.5	1.8	582	2	T51625	MAP3K alpha protei
1091	74.5	1.8	590	2	G71136	probable transport
1092	74.5	1.8	597	1	P2IVTV	RNA-directed RNA p
1093	74.5	1.8	598	2	A57249	beta-galactosidase
1094	74.5	1.8	626	2	S53871	Pmel 17 protein -
1095	74.5	1.8	640	2	H83267	probable ATP-bindi
1096	74.5	1.8	656	2	H86400	protein T17H3.7 [i

1097	74.5	1.8	675	2	F87022	penicillin-binding
1098	74.5	1.8	682	1	KIBOGC	protein kinase C (
1099	74.5	1.8	684	2	S45758	proliferating-cell
1100	74.5	1.8	702	2	AG0005	guanosine-3',5'-bi
1101	74.5	1.8	706	2	F87683	peptidase M13 fami
1102	74.5	1.8	706	2	S61717	probable membrane
1103	74.5	1.8	715	2	I40729	hypothetical 76K p
1104	74.5	1.8	717	2	T29816	hypothetical prote
1105	74.5	1.8	760	2	AC0613	formate acetyltran
1106	74.5	1.8	762	2	T00410	protein kinase hom
1107	74.5	1.8	767	2	F71479	hypothetical prote
1108	74.5	1.8	775	2	T00962	hypothetical prote
1109	74.5	1.8	782	2	T43277	host cell factor 1
1110	74.5	1.8	808	2	G86208	protein F22G5.28 [
1111	74.5	1.8	837	2	T00355	hypothetical prote
1112	74.5	1.8	858	2	S50730	hypothetical prote
1113	74.5	1.8	858	2	T00258	hypothetical prote
1114	74.5	1.8	872	2	S51620	Ost oncogene - rat
1115	74.5	1.8	884	2	T20405	hypothetical prote
1116	74.5	1.8	897	2	S50550	SIN1-associated pr
1117	74.5	1.8	923	2	S09583	peptidylglycine mo
1118	74.5	1.8	949	1	S55478	pyruvate, phosphat
1119	74.5	1.8	974	2	T04910	hypothetical prote
1120	74.5	1.8	976	1	URRTAP	peptidylglycine mo
1121	74.5	1.8	993	2	T17230	hypothetical prote
1122	74.5	1.8	1045	2	T41119	internalin- relate
1123	74.5	1.8	1050	1	A57134	1-phosphatidylinos
1124	74.5	1.8	1164	2	S71792	phosphatidylinosit
1125	74.5	1.8	1227	2	T50394	DNA-directed RNA p
1126	74.5	1.8	1260	2	T01334	hypothetical prote
1127	74.5	1.8	1324	2	T17468	peptide-synthetase
1128	74.5	1.8	1331	2	T29249	hypothetical prote
1129	74.5	1.8	1462	2	T42639	glucocorticoid rec
1130	74.5	1.8	1556	2	D36793	hypothetical prote
1131	74.5	1.8	1616	2	I37183	gene APXL protein
1132	74.5	1.8	1997	2	T30874	virginiamycin S sy
1133	74.5	1.8	2183	2	T42764	coagulation factor
1134	74.5	1.8	2247	2	T16637	hypothetical prote
1135	74.5	1.8	2254	2	T09053	low voltage-activa
1136	74.5	1.8	2314	1	A46151	protein-tyrosine-p
1137	74.5	1.8	2535	2	T04824	hypothetical prote
1138	74.5	1.8	3069	2	H70656	fatty-acid synthas
1139	74.5	1.8	3122	2	T17202	DNA-directed DNA p
1140	74.5	1.8	3175	1	RRWVEV	genome polyprotein
1141	74.5	1.8	3570	2	T45025	mucin MUC5B, trach
1142	74.5	1.8	4151	2	G70944	probable polyketid
1143	74.5	1.8	4342	2	H83343	probable non-ribos
1144	74.5	1.8	15281	2	S41309	cyclosporin synthe
1145	74	1.8	156	2	AB1889	hypothetical prote
1146	74	1.8	158	2	F69741	gltX 5'-region con
1147	74	1.8	213	2	S26844	type II site-speci
1148	74	1.8	213	2	A38693	BamHI endonuclease
1149	74	1.8	231	2	B49934	phosphoglycolate p
1150	74	1.8	237	2	S77151	sugar fermentation
1151	74	1.8	308	2	E72670	hypothetical prote
1152	74	1.8	337	2	G87487	conserved hypothet
1153	74	1.8	344	2	JC5601	cAMP response elem

1154	74	1.8	348	2	T39036	hypothetical prote
1155	74	1.8	352	2	S09266	Ig alpha chain C r
1156	74	1.8	366	2	T05807	hypothetical prote
1157	74	1.8	376	2	T02938	6-phosphofructo-2-
1158	74	1.8	376	2	C87596	glycosyl hydrolase
1159	74	1.8	392	2	S04205	protein-tyrosine k
1160	74	1.8	398	2	B70752	hypothetical prote
1161	74	1.8	414	2	JU0292	streptokinase - St
1162	74	1.8	414	2	S75052	hypothetical prote
1163	74	1.8	425	2	B71038	probable Na ⁺ /H ⁺ -ex
1164	74	1.8	448	2	B69745	phosphoglucomutase
1165	74	1.8	449	2	C95332	probable copper-co
1166	74	1.8	465	2	F95333	hypothetical prote
1167	74	1.8	467	2	A45629	cysteine proteinas
1168	74	1.8	478	2	A47693	putrescine oxidase
1169	74	1.8	502	2	AD3160	hypothetical prote
1170	74	1.8	507	2	S54303	zinc transport pro
1171	74	1.8	512	1	TVHULY	protein-tyrosine k
1172	74	1.8	523	2	A42301	anthranilate synth
1173	74	1.8	525	2	H83294	hypothetical prote
1174	74	1.8	557	2	T39308	asparagine synthas
1175	74	1.8	560	2	S09995	nuclear factor I-B
1176	74	1.8	565	2	B70652	probable cysG prot
1177	74	1.8	585	2	AG0955	conserved hypothet
1178	74	1.8	596	2	F88188	protein C18H9.7 [i
1179	74	1.8	610	2	T28856	hypothetical prote
1180	74	1.8	626	2	E70747	hypothetical prote
1181	74	1.8	632	2	JC7155	brain finger prote
1182	74	1.8	633	2	T17262	hypothetical prote
1183	74	1.8	649	1	S58097	probable dna repai
1184	74	1.8	663	2	F84490	probable TNP2-like
1185	74	1.8	681	2	C75395	methionyl-tRNA syn
1186	74	1.8	685	2	T40162	transketolase - fi
1187	74	1.8	710	2	T49516	Atu related protei
1188	74	1.8	725	2	T20526	glutamine-fructose
1189	74	1.8	749	2	S75331	penicillin-binding
1190	74	1.8	749	2	B86606	primosomal protein
1191	74	1.8	749	2	C72018	primosomal protein
1192	74	1.8	752	2	B65070	probable oxidoredu
1193	74	1.8	761	2	T51912	hypothetical prote
1194	74	1.8	764	2	A45321	protein-glutamine
1195	74	1.8	769	1	QRRTGS	secretory componen
1196	74	1.8	790	1	A48356	genome polyprotein
1197	74	1.8	823	2	AF3361	endopeptidase La (
1198	74	1.8	838	2	T47828	hypothetical prote
1199	74	1.8	850	2	JC5047	ras GTPase-activat
1200	74	1.8	852	2	S29358	pol protein - bovi
1201	74	1.8	918	2	A41667	nitrate reductase
1202	74	1.8	940	2	A40985	projectin - fruit
1203	74	1.8	942	2	C96589	hypothetical prote
1204	74	1.8	948	2	T47322	plasma membrane H ⁺
1205	74	1.8	1002	1	GNWXCS	genome polyprotein
1206	74	1.8	1066	2	S72479	Nuc-2 protein - Ne
1207	74	1.8	1112	2	T30202	probable chitin sy
1208	74	1.8	1181	2	E83658	transcription-repa
1209	74	1.8	1203	2	T28895	hypothetical prote
1210	74	1.8	1219	2	T14578	nucleoporin Nup153

1211	74	1.8	1221	2	T23472	hypothetical prote
1212	74	1.8	1243	2	T17390	vrlK protein - Dic
1213	74	1.8	1285	2	T14171	ataxin-2 - mouse
1214	74	1.8	1305	2	D82923	DNA-directed RNA p
1215	74	1.8	1310	2	S30328	multidrug resistan
1216	74	1.8	1320	2	AE0633	proline dehydrogen
1217	74	1.8	1345	2	T00964	hypothetical prote
1218	74	1.8	1406	2	AB0456	DNA-directed RNA p
1219	74	1.8	1443	2	G75393	hypothetical prote
1220	74	1.8	1589	1	RGBYC5	cell division cont
1221	74	1.8	1632	2	C70752	probable ctpI prot
1222	74	1.8	1641	2	D82704	conserved hypothet
1223	74	1.8	1692	2	G01449	probable mucin G2
1224	74	1.8	1762	2	T03222	probable polyketid
1225	74	1.8	1773	2	T05128	hypothetical prote
1226	74	1.8	1784	2	T10532	gag-pol polyprotei
1227	74	1.8	2059	2	D82671	surface protein XF
1228	74	1.8	2228	2	T14029	variant-specific s
1229	74	1.8	2233	2	T28669	surface protein 5l
1230	74	1.8	2325	2	T02235	acetyl-CoA carboxy
1231	74	1.8	2468	2	A83412	hypothetical prote
1232	74	1.8	2655	2	D96595	probable acetyl-Co
1233	74	1.8	3084	1	MMMSA	laminin alpha-1 ch
1234	74	1.8	3149	1	QQBE8	BPLF1 protein - hu
1235	74	1.8	5032	1	A35041	ryanodine receptor
1236	74	1.8	6260	2	T30228	polyketide synthas
1237	73.5	1.8	209	2	E97285	ribosomal protein
1238	73.5	1.8	260	2	E81194	biotin synthesis p
1239	73.5	1.8	279	2	S75971	hypothetical prote
1240	73.5	1.8	311	1	A64623	thioredoxin-disulf
1241	73.5	1.8	312	2	S34635	superantigen Mtv -
1242	73.5	1.8	334	1	S15318	transcription regu
1243	73.5	1.8	348	2	S16898	recombination prot
1244	73.5	1.8	359	2	A42462	acetoin catabolism
1245	73.5	1.8	361	2	T49587	7alpha-cephem-meth
1246	73.5	1.8	362	2	D84713	probable dioxygena
1247	73.5	1.8	388	2	H72625	probable acetylorn
1248	73.5	1.8	391	2	T36739	hypothetical prote
1249	73.5	1.8	396	2	D26956	translation elonga
1250	73.5	1.8	403	1	S35541	transcription fact
1251	73.5	1.8	410	2	D75475	lycopene cyclase -
1252	73.5	1.8	431	1	JC2002	transcription fact
1253	73.5	1.8	436	1	S49458	diphosphate-fructo
1254	73.5	1.8	460	2	G83421	cysteinyl-tRNA syn
1255	73.5	1.8	466	2	S62332	beta-fructofuranos
1256	73.5	1.8	473	2	T48985	hypothetical prote
1257	73.5	1.8	480	2	A31589	carboxypeptidase C
1258	73.5	1.8	488	2	S40706	hypothetical prote
1259	73.5	1.8	491	2	A39302	cytochrome P450 50
1260	73.5	1.8	519	2	T24772	hypothetical prote
1261	73.5	1.8	529	2	JQ0783	55.5K sporulation
1262	73.5	1.8	542	2	T00887	protein kinase hom
1263	73.5	1.8	544	2	B84264	glycine betaine tr
1264	73.5	1.8	548	2	F90918	fumarase A [import
1265	73.5	1.8	548	2	C85767	fumarase A [simila
1266	73.5	1.8	571	2	H87600	hypothetical prote
1267	73.5	1.8	579	2	B45266	MPL-K protein prec

1268	73.5	1.8	580	2	A83874	carbon starvation-
1269	73.5	1.8	610	2	F88109	protein T24E12.9 [
1270	73.5	1.8	615	2	T35569	glutamine-fructose
1271	73.5	1.8	622	2	G96703	unknown protein, 3
1272	73.5	1.8	655	2	T39064	RNA binding protei
1273	73.5	1.8	700	2	S09699	bib protein - frui
1274	73.5	1.8	704	2	B84530	probable RING zinc
1275	73.5	1.8	706	2	S70665	catalase (EC 1.11.
1276	73.5	1.8	727	2	E83916	malate synthase BH
1277	73.5	1.8	737	1	S14408	translation elonga
1278	73.5	1.8	756	2	AB1088	chitinase B homolo
1279	73.5	1.8	769	2	S36657	SWI6 protein - yea
1280	73.5	1.8	841	2	JC5894	killer cell inhibi
1281	73.5	1.8	862	2	T05941	lipoxygenase (EC 1
1282	73.5	1.8	886	2	AD0831	probable acyl-CoA
1283	73.5	1.8	961	2	T03467	NADH dehydrogenase
1284	73.5	1.8	966	2	T50668	villin 3 [imported
1285	73.5	1.8	997	2	A60776	230k bullous pemph
1286	73.5	1.8	1021	2	AG1938	hypothetical prote
1287	73.5	1.8	1038	2	AG2187	hypothetical prote
1288	73.5	1.8	1095	2	S76044	hypothetical prote
1289	73.5	1.8	1122	1	NCECXV	exodeoxyribonuclea
1290	73.5	1.8	1180	2	G85933	DNA helicase RecB
1291	73.5	1.8	1180	2	E91088	DNA helicase RecB
1292	73.5	1.8	1199	1	GNMV1M	HIV-1 retropepsin
1293	73.5	1.8	1216	2	A55620	apical endosomal p
1294	73.5	1.8	1242	2	AB0672	respiratory nitrat
1295	73.5	1.8	1268	2	S33411	botulinum neurotox
1296	73.5	1.8	1273	2	T38292	hypothetical prote
1297	73.5	1.8	1484	2	T42632	breast cancer tumo
1298	73.5	1.8	1513	2	A54895	mucin 2, intestina
1299	73.5	1.8	1602	2	H70984	probable polyketid
1300	73.5	1.8	1609	2	A86611	probable outer mem
1301	73.5	1.8	1609	2	H72013	polymorphic membra
1302	73.5	1.8	1657	2	T15838	hypothetical prote
1303	73.5	1.8	1802	2	S69703	HKR1 protein precu
1304	73.5	1.8	2321	2	S78549	notch3 protein - h
1305	73.5	1.8	2480	2	D84904	hypothetical prote
1306	73.5	1.8	2718	2	A23475	G surface protein
1307	73.5	1.8	2910	2	T42214	otogelin - mouse
1308	73.5	1.8	6658	2	T13931	projectin - fruit
1309	73	1.8	202	2	H87154	dTDP-4-dehydrorham
1310	73	1.8	224	2	A75610	transcription regu
1311	73	1.8	304	2	G83230	probable transcrip
1312	73	1.8	305	2	S44907	ZK652.5 protein -
1313	73	1.8	313	2	JC5475	pollen allergen 9
1314	73	1.8	331	2	E84770	probable serpin [i
1315	73	1.8	340	2	S62493	replication factor
1316	73	1.8	347	2	AC0593	quinolinate synthe
1317	73	1.8	362	2	T45072	erythroid Kruppel-
1318	73	1.8	364	2	I45915	interstitial retin
1319	73	1.8	365	2	I57814	MHC class I-alpha
1320	73	1.8	369	2	F95904	hypothetical prote
1321	73	1.8	370	2	AG0359	probable membrane-
1322	73	1.8	372	2	A43638	lignin peroxidase
1323	73	1.8	382	2	D69304	probable acyl-CoA
1324	73	1.8	384	2	S74774	hypothetical prote

1325	73	1.8	406	2	AH0563	fosmidomycin resis
1326	73	1.8	407	2	T19155	hypothetical prote
1327	73	1.8	408	2	T08400	late embryonic abu
1328	73	1.8	408	2	AC0961	probable ATP/GTP-b
1329	73	1.8	408	2	AI0813	probable membrane
1330	73	1.8	411	1	OXRTL	protein-lysine 6-o
1331	73	1.8	421	2	A83933	hypothetical prote
1332	73	1.8	423	2	E81000	phosphoribosylamin
1333	73	1.8	434	2	S77607	glutamate/glutamin
1334	73	1.8	440	2	E87406	preprotein translo
1335	73	1.8	449	2	D86231	hypothetical prote
1336	73	1.8	451	2	AE0831	CDPdiacylglycerol-
1337	73	1.8	457	2	F64095	argininosuccinate
1338	73	1.8	458	2	H82051	argininosuccinate
1339	73	1.8	464	2	D75204	site specific DNA-
1340	73	1.8	466	2	T43727	fumarate hydratase
1341	73	1.8	466	2	T49756	related to berberi
1342	73	1.8	472	2	F82143	hypothetical prote
1343	73	1.8	474	2	T00943	hypothetical prote
1344	73	1.8	482	2	S30159	N-formimidoyl fort
1345	73	1.8	492	2	S10395	catalase (EC 1.11.
1346	73	1.8	494	2	T05302	vacuolar processin
1347	73	1.8	503	2	S54302	zinc transporter Z
1348	73	1.8	509	2	S18872	legumin-like stora
1349	73	1.8	509	2	T31136	multidrug-efflux t
1350	73	1.8	518	2	T45765	hypothetical prote
1351	73	1.8	526	2	F85086	hypothetical prote
1352	73	1.8	528	2	G70755	probable choline d
1353	73	1.8	536	2	D83419	probable ATP-bindi
1354	73	1.8	545	2	D87259	phosphoglucomutase
1355	73	1.8	551	2	I46709	endothelial leukoc
1356	73	1.8	553	2	C84920	hypothetical prote
1357	73	1.8	557	2	T07116	protoporphyrinogen
1358	73	1.8	576	1	NDBSR1	type II site-speci
1359	73	1.8	609	2	A49839	odd-paired - fruit
1360	73	1.8	612	2	C90419	glucan 1,4 alpha g
1361	73	1.8	616	2	T08708	hypothetical prote
1362	73	1.8	624	2	JC5471	regulatory protein
1363	73	1.8	624	2	T02562	probable salt-indu
1364	73	1.8	638	2	D69957	conserved hypothet
1365	73	1.8	656	2	T37941	conserved hypothet
1366	73	1.8	662	2	H95934	probable MPAl fami
1367	73	1.8	673	2	G83961	ATP-dependent DNA
1368	73	1.8	687	2	S53485	carnitine O-acetyl
1369	73	1.8	691	2	S41008	hypothetical prote
1370	73	1.8	693	2	S64904	probable membrane
1371	73	1.8	703	2	G75638	nodulation protein
1372	73	1.8	707	1	A53796	gelatinase B (EC 3
1373	73	1.8	730	2	B86282	protein F10B6.22 [
1374	73	1.8	731	2	F82286	phosphate ABC tran
1375	73	1.8	734	2	B82959	hypothetical prote
1376	73	1.8	739	2	H85245	VP1 like protein [
1377	73	1.8	739	2	T05163	hypothetical prote
1378	73	1.8	742	2	T47453	oxidosqualene cycl
1379	73	1.8	747	1	S36741	probable copper-tr
1380	73	1.8	756	2	G86150	F22M8.3 protein -
1381	73	1.8	764	2	T21128	hypothetical prote

1382	73	1.8	770	2	A91052	penicillin binding
1383	73	1.8	775	2	I49237	A20 protein - mous
1384	73	1.8	775	2	I49759	hepatocyte growth
1385	73	1.8	784	2	B86303	hypothetical prote
1386	73	1.8	787	2	C81166	phenylalanyl-tRNA
1387	73	1.8	791	2	A46616	cytochrome-c oxida
1388	73	1.8	808	2	D88564	protein T05G5.8 [i
1389	73	1.8	818	1	RRVGCR	RNA-directed RNA p
1390	73	1.8	832	1	S20757	DNA-directed DNA p
1391	73	1.8	845	1	JDVLVD	DNA-directed DNA p
1392	73	1.8	849	2	D88368	protein F19H8.4 [i
1393	73	1.8	852	2	A85041	probable receptor
1394	73	1.8	879	2	F96558	probable protein k
1395	73	1.8	881	2	C87471	TonB-dependent rec
1396	73	1.8	885	2	AD2077	hypothetical prote
1397	73	1.8	986	2	T52176	aldehyde oxidase (
1398	73	1.8	993	2	A96750	hypothetical prote
1399	73	1.8	1004	2	T30338	oviductin (EC 3.4.
1400	73	1.8	1023	2	T30257	IgG Fc binding pro
1401	73	1.8	1087	2	T49496	hypothetical prote
1402	73	1.8	1099	2	AE1065	conserved hypothet
1403	73	1.8	1100	2	T42260	guanylate cyclase
1404	73	1.8	1116	2	T42213	m-tomosyn, isoform
1405	73	1.8	1189	2	T17088	homeodomain-intera
1406	73	1.8	1199	2	T18522	tubulin-folding co
1407	73	1.8	1254	2	I48161	p-185 precursor -
1408	73	1.8	1418	2	S40764	hypothetical prote
1409	73	1.8	1520	2	AF3008	polyketide synthas
1410	73	1.8	1520	2	G98275	hypothetical prote
1411	73	1.8	1587	2	AB2012	hypothetical prote
1412	73	1.8	1774	2	T17421	polyketide synthas
1413	73	1.8	1776	1	RRWPYM	genome polyprotein
1414	73	1.8	2076	2	S15999	fatty-acyl-CoA syn
1415	73	1.8	2083	2	T42721	CRP-ductin-alpha p
1416	73	1.8	2103	2	G86925	probable polyketid
1417	73	1.8	2123	2	F86348	hypothetical prote
1418	73	1.8	2514	1	MNWWN2	nonstructural poly
1419	73	1.8	2588	2	T14342	NSD1 protein - mou
1420	73	1.8	3014	1	JC5620	genome polyprotein
1421	73	1.8	3530	2	A59266	unconventional myo
1422	73	1.8	3562	2	A47171	chondroitin sulfat
1423	73	1.8	3660	1	S02041	dystrophin, muscle
1424	73	1.8	4558	2	C82199	RTX toxin RtxA VC1
1425	73	1.8	9376	2	T14593	syringomycin synth
1426	72.5	1.8	195	2	C75254	3-octaprenyl-4-hyd
1427	72.5	1.8	234	2	S60183	protein ExsB - Rhi
1428	72.5	1.8	252	2	H72469	hypothetical prote
1429	72.5	1.8	283	2	G84458	probable protein p
1430	72.5	1.8	294	2	T35191	probable DNA hydro
1431	72.5	1.8	301	2	AB3216	dihydrodipicolinat
1432	72.5	1.8	316	2	D85709	hypothetical prote
1433	72.5	1.8	317	2	B87298	metallo-beta-lacta
1434	72.5	1.8	347	2	F97223	uncharaterized con
1435	72.5	1.8	354	2	T46014	squamosa promoter-
1436	72.5	1.8	357	2	S09269	Ig alpha chain C r
1437	72.5	1.8	371	2	AG1088	lipase homolog lmo
1438	72.5	1.8	372	2	I58141	ciliary neurotroph

1439	72.5	1.8	377	2	D70957	hypothetical prote
1440	72.5	1.8	378	1	S74758	probable hydro-ly
1441	72.5	1.8	379	2	AF11191	B. subtilis YhbA p
1442	72.5	1.8	390	2	B85910	unknown protein en
1443	72.5	1.8	390	2	T09914	protein-arginine N
1444	72.5	1.8	397	2	S27600	N-acetylglutamate
1445	72.5	1.8	402	1	JU0332	alkaline proteinas
1446	72.5	1.8	413	2	S65948	hemolin - cecropia
1447	72.5	1.8	426	2	F90648	glutamate-1-semial
1448	72.5	1.8	426	2	F85499	glutamate-1-semial
1449	72.5	1.8	444	1	G70349	DNA repair protein
1450	72.5	1.8	459	2	AH2426	glutathione reduct
1451	72.5	1.8	470	2	S22080	Ig heavy chain pre
1452	72.5	1.8	476	2	E81849	Glu-tRNAGln amidot
1453	72.5	1.8	476	2	T48399	heat shock transcr
1454	72.5	1.8	483	2	S52226	cobQ protein - Rho
1455	72.5	1.8	503	2	AC3148	exopolysaccharide
1456	72.5	1.8	504	2	AG1847	anthranilate synth
1457	72.5	1.8	504	2	S54744	cellulase (EC 3.2.
1458	72.5	1.8	507	1	UFRT	fumarate hydratase
1459	72.5	1.8	512	1	I56160	protein-tyrosine k
1460	72.5	1.8	512	2	F85342	beta-1, 3-glucanas
1461	72.5	1.8	518	2	D96828	hypothetical prote
1462	72.5	1.8	533	1	JU0146	serine proteinase
1463	72.5	1.8	538	2	T51756	NAD+ synthase (glu
1464	72.5	1.8	545	2	T08564	hypothetical prote
1465	72.5	1.8	548	1	B44511	fumarate hydratase
1466	72.5	1.8	550	2	H98139	gumJ protein [impo
1467	72.5	1.8	554	2	D72760	hypothetical prote
1468	72.5	1.8	566	2	S22477	vicilin precursor
1469	72.5	1.8	570	2	S56132	cellulase (EC 3.2.
1470	72.5	1.8	580	2	F81042	hemolysin activati
1471	72.5	1.8	584	2	S77647	mobilisation prote
1472	72.5	1.8	584	2	F84425	hypothetical prote
1473	72.5	1.8	591	2	I38924	reduced folate car
1474	72.5	1.8	592	2	JN0877	protein kinase C (
1475	72.5	1.8	594	2	E83847	two-component sens
1476	72.5	1.8	607	2	S70106	probable arginine-
1477	72.5	1.8	613	2	A82834	hypothetical prote
1478	72.5	1.8	614	2	S27962	modulator recognit
1479	72.5	1.8	617	2	E90851	hypothetical prote
1480	72.5	1.8	617	2	B91066	hypothetical prote
1481	72.5	1.8	620	2	AE2325	NADH dehydrogenase
1482	72.5	1.8	628	2	S01955	hypothetical prote
1483	72.5	1.8	645	2	G01205	TYL protein - huma
1484	72.5	1.8	647	2	JE0337	Frizzled-1 protein
1485	72.5	1.8	658	2	T32053	hypothetical prote
1486	72.5	1.8	662	2	AB1979	calcium-dependent
1487	72.5	1.8	681	2	E70942	hypothetical prote
1488	72.5	1.8	697	1	S04987	SITS-binding prote
1489	72.5	1.8	723	2	AG1603	polynucleotide pho
1490	72.5	1.8	726	2	H86205	hypothetical prote
1491	72.5	1.8	756	2	S60966	probable protein k
1492	72.5	1.8	779	2	E97778	endopeptidase La (
1493	72.5	1.8	779	2	B84866	hypothetical prote
1494	72.5	1.8	792	2	S32244	X-Pro dipeptidyl-p
1495	72.5	1.8	812	1	A36477	fibroblast growth

ALIGNMENTS

C;Superfamily: semaphorin

Qy	1	MALPALGLDPWSLLGLFLFQLQLLLPT--TTAGGGGQGPMPrVRYAGDERRALSFFHQ	58
Db	1	MALPSLGQDSWSLLRVFFFQL--FLLPSLPASGTGGQGPMPrVKYHAGDGHRLSFFQQ	58
Qy	59	KGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGPRLKNMIPWPASDRKKSECAFKKK	118
Db	59	KGLRDFDTLLLSDDGNTLYVGARETVLALNIQNPGIPRLKNMIPWPASERKKTECAFKKK	118
Qy	119	SNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPF	178
Db	119	SNETQCFNFIRVLVSYNATHLYACGTFAFSPACTFIELQDSLLLPIIDKVMGKGQSPL	178
Qy	179	DPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIP	238
Db	179	TLFTSTQAVLVDGMLYSGTMNFLGSEPILMRTLGSHPVLKTDIFLRWLHADASFVAAIP	238
Qy	239	STQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ	298
Db	239	STQVVYFFFEETASEFDFFEELYISRVAQVCKNDVGGEKLLQKKWTTFLKAQLLCAQPGQ	298
Qy	299	LPFNVIIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELN	358

Db	299	LPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLTDIERVFKGKYKELN	358
Qy	359	KETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRL	418
Db	359	KETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFMLDEHVVGTPLLVKSGVEYTRL	418
Qy	419	AVETAQGLDGHSHLVMYLGTGTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQ	478
Db	419	AVESARGLDGSSHVMYLGSTGTLPHKAVVPQDSSAYLVEEIQLSPDSEPVRNLQLAPAQ	478
Qy	479	GAVFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDM	538
Db	479	GAVFAGFSGGIWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCLLSG-STKPKWKQDM	537
Qy	539	ERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAV	598
Db	538	ERGNPEWVCTRGPMARSPRRQSPQLIKEVLTVPNSILELRCPHLSALASYHWSHGAKI	597
Qy	599	PEASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPR	658
Db	598	SEASATVYNGSLLLLPQDGVGGLYQCVATENGYSYPVVSYWVDSQDQPLALDPELAGVPR	657
Qy	659	EHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFLVLGALIIILVASPLRALRARGKVQG	718
Db	658	ERVQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIVLLGVLTLLLASPLGALRARGKVQG	717
Qy	719	CETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	718	CGMLPPREKAPLSRDOHLQPSKDHRTSASDVDADNNHLGAEVA	760

I48746

C;Species: Mus musculus (house mouse)

C;Accession: I48746

Neuron 14, 941-948, 1995

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-782 <RES>

C; Genetics:

C;Superfamily: semaphorin

Qy 49 ERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP--RLKNMIPWPAS 106

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      | | : | : : : | | | | | | | | : | : : | |
Db      1 EERLIRKFEAENISNYTALLLSQDGKTLVYGAREALFALNSNLSFLPGGEYQELL-WSAD 59
Qy      107 DRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISE 166
      : | : | : | | : | | : : : | : | | | | | | | : | : |
Db      60 ADRKQQCSFKGKDPKRDCQNYIKILLPLNSSHLLTCGTAAFSPLCAYIHIAFSTLAQDEA 119
Qy      167 DKVM--EGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFL 224
      | : : | | | | | | | | : | : | | | : | : | : | : |
Db      120 GNVILEDGKGHCPCFDPNFKSTALVVDGELYTGTVSSFQGNPAISRSQSSRPT-KTESSL 178
Qy      225 RWLHHDASFVAAPSTQ-----VVYFFFEETASEFDFFERLHTRSRRVARVCKNDVG 274
      | | | : | | : | : : : | | | | | | | | : | | | | | | |
Db      179 NWL-QDPAFVASATSPESLGSPIGDDDKIYFFFSETGQEFEFFENTIVSRVARVCKGDEG 237
Qy      275 GEKLLQKKWTTFLKAQLLCTQPGQ-LPFNVIRHAVLL---PADSPTAPHIYAVFTSQWQV 330
      | | : : | | : | | | | | | : | | | : : | | | | | | |
Db      238 GERVLQQRWTSFLKAQLLCSRPDGFPFNVLQDVFTLNPNPQDWRKTLSTI-GVFTSQWHR 296
Qy      331 GGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPS----- 384
      | | | | : | | : : : | | | : : | | : | | | | : |
Db      297 GTTEGSAICVFTMNDVQKAFDGLYKKVNRETQQWYTETHQVPTPRPGACITNSARERKIN 356
Qy      385 -----SDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAVETAQGLDGHS-HLVMYLGT 438
      | : | | : | | | | | | | | | : : | | : | | | | : | : | |
Db      357 SSLQLPDRVLNFKDHFMDGQVRSRLLLQLPRARYQRVAVHRVPGL--HSTYDVLFLGT 414
Qy      439 TTGSLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCS 498
      | | | | | | | | | : : | | : | : | | | | : : | | : | | | |
Db      415 GDGRHLKAVTL-SSRVHIIELQIFPQGQPVQNLLLDHGGGLLYASSHSGVVQVPVANCS 473
Qy      499 VYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNS--WKQDMERGNPEWACASGPMSRSL 556
      : | : | | : | | | : | | : | | | | | | : : | :
Db      474 LYPTCGDCLLARDPYCAWTGSACRLASLYQPDLASRPWTQDIEGASVKELCKNSSYKARF 533
Qy      557 RPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAPPEASS--TVYNGSLLLI- 613
      : | | : | | | : | | | | | : | | | : | : | | | :
Db      534 LVPGKP--CKQVQIQPNTVNTLACPLLSNLATRLWVHNGAPVNASASCRVLPDGLLLVG 591
Qy      614 VQDGVGGLYQCWATENGFSYPVISYWVDSQDQ-TLALDPELAGIPREHVKVPLTRVS--- 669
      | | : | : | | : | | | | : : : : | | | : | |
Db      592 SQQGL-GVFQCWSIEEGFQQLVASYCPEVMEEGVMDQKNQRDGRP---VIINTSRVSAPA 647
Qy      670 -GGAALAAQQSYWPHFVTVTVL--FALVL 695
      | : | : | | | : : | | | : |
Db      648 GGRDSWGADKSYWNEFLVMCTLFVFAMVL 676

```

RESULT 3

S66498

M-sema F protein precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S66498

R;Inagaki, S.; Furuyama, T.; Iwahashi, Y.

FEBS Lett. 370, 269-272, 1995

A;Title: Identification of a member of mouse semaphorin family.

F;22-834/Product: M-sema F protein #status predicted <MAT>

Matches 271; Conservative 115; Mismatches 242; Indels 137; Gaps 25;

Qy	39	MPRVRYAYAGDERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAAREAILALDIQDPGVPRLK	98
Db	28	: : : : : : : : : :	
Qy	28	VPRKTVSSGSELVTVVRRFSQTGIQDFLTTLTEHSGLLYVGAREALFAFSVE---ALELQ	84
Qy	99	NMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQD	158
Db	85	: : : : : :	
Qy	85	GAISWEAPAEEKKIECTQKGKSNQTECFNFIRFLQPYNSSHLYVCCTYAFQPKCTYINM--	142
Qy	159	SYLLPISEDKVMGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVL	218
Db	143	: : : : : : : : : : : : :	
Qy	143	-LTFTLDRAEFEDGKGKCPYDPAKGHTGLLVDGELYSATLNNFLGTPEVILRYMGTHHSI	201
Qy	219	KTDNFLRWLHHDASFV--AAIPST-----QVVYFFFEETASEDFFERLHTSRVARV	268
Db	202	: : : : : : : : :	
Qy	202	KTEYLAFWL-NEPHFVGSAFVPESVGSFTGDDDKIYFFFSERAVEYDCYSEQVVARVARV	260
Qy	269	CKNDVGGEKLLQKKWTTFLKAQLLCTQPG-QLPFNVIRHAVLLPADSPTAPHIYAVFTSQ	327
Db	261	: : : : : : : : : : :	
Qy	261	CKGDMGGARTLQKKWTTFLKARLVCSAPDWKVYFNQLKAVHTLRGASWHNTTFFGVFQAR	320
Qy	328	WQVGGRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SV	381
Db	321	: : : : : : : : : :	
Qy	321	W--GDMDLSAVCEYQLEQIQQVFEGPYKEYSEQAQKWARYTDPVPSRPGSCINNWHRDN	378
Qy	382	GPSS-----DKALTFMKDHFLLMDEQV---VGTPLLVKSGVEYTRLAVETAQGLDGHSHLV	433
Db	379	: : : : : : : : : :	
Qy	379	GYTSSLELPDNTLNFIIKKHPLMEDQVKPRLGRPLLVKNTNFTHVVADRPGLDGATYTV	438
Qy	434	MYLGTTTGSLLHKAUVSGDSSAHLVEEIQLPDPPEPVRNLQLAPTQGAVFVGFSGGVWRVP	493
Db	439	: : : : : : : : : : : :	
Qy	439	LFIGTGDGWLLKAVSLG-PWIHMVEELQVF-DQEPVESLVLSQSKKVLFAGSRSQVLQLS	496
Qy	494	RANCSVYESCVDCVLARDPHCAWDPEsrTCCLLSA-----PNLNSWKQDMERGN	542
Db	497	: : : : : : : : : : : :	
Qy	497	LADCTKYRFCVDCVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYG-	555
Qy	543	PEWACASGPMsRLRPQSRPQIIKEVLAVPNSI-----LELPCPHLSA-LASYWWSHG	594
Db	556	: : : : :	
Qy	556	-----IKKVRsIPKNITVVSgTDLVLPC-HLSSNLAHAHWTFG	592
Qy	595	PAAVP--EASSTVYNGSLLLIV----QDGVGGLYQCWATENGFSYPVISYW---VDSQDQ	645
Db		: : : : : : : : : : : : : :	

```

Db      593 SQDLPAEQPGSFLYDTGLQALVVMMAQSRHSGPYRCYSEEQGTRLAAESYLVAVVAGSSV 652
Qy      646 TLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAVLVLSGA----LII 701
      ||                      : || :                      | |:| || |::
Db      653 TL-----EAPLENLG-----LVWLAVVALGAVCLVLLL 682
Qy      702 LVASPLRALRARGKVQGCELTLPGEKA-----PLSREQHLQSP 739
      || | | ||          | | | ||          || : ||
Db      683 LVLSLRRRLR-----EELEKGAKASERTLVYPLELPKEPASP 719

```

RESULT 4

G02173

semaphorin III family homolog - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999

C;Accession: G02173

R;Naylor, S.

submitted to the EMBL Data Library, October 1995

A;Reference number: G09275

A;Accession: G02173

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-753 <NAY>

A;Cross-references: EMBL:U38276; NID:g1061350; PIDN:AAB18276.1; PID:g1061351

C;Superfamily: semaphorin

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Query Match          20.8%; Score 838.5; DB 2; Length 753;
Best Local Similarity 31.5%; Pred. No. 5.6e-58;
Matches 230; Conservative 114; Mismatches 279; Indels 107; Gaps 30;

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Qy      26 LPTTTAGGGGQGPMPRVRYAGDERRALSFFHQK-----GLQDFDTLLLSGDG 73
      || |          |||          || |          | : | | |
Db      26 LPAT-----PRVR-----LSFKELKATGTAHFFNLLNTDYRIILKDEDH 66
Qy      74 NTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQCFNFIRVLVS 133
      : :|||::: :|:|: | : | :| | || :: | | :| ||:|::
Db      67 DRMYVGSKDYVLSLDLHD--INREPLIIHWAASPQRIEECVLSGKDVNGECGNFVRLIQP 124
Qy      134 YNVTHLYTCGTFAFSPACTFI----ELQDSYLLPISEDKVMGKGQSPFDPAHKHTAVLV 189
      :| ||| | || |::| ||: || | : : : ||| :| || : | :
Db      125 WNRTHLYVCGTGAYNPMCTYVNRGRRAQD-YIFYLEPERLESKGKCPYDPKLDTASALI 183
Qy      190 DGMLYSGTMNPNFLGSEPILMRTLGSQPVLKTDNF-LRWLHHDASFVAA--IPST----QV 242
      : ||:| :|:|:: : ||| | :|| : ||| :| ||: | || :
Db      184 NEELYAGVYIDFMGTDAALFRTLKGQTAMRTDQYNSRWL-NDPSFIHAELIPDSAENDDK 242
Qy      243 VYFFFEETASEFDFFERLHTRSARVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG----Q 298
      :||| | :| : : :|: | :| || | ||:| ||| :| :| :
Db      243 LYFFFRERSAEAPQSPAVY-ARIGRICLNDDGGHCCLVNKKWSTFLKARLVCSVPGEDGIE 301
Qy      299 LPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELN 358
      |: :: : | ||||| | | ||| :|: || || | :
Db      302 THFDELQDVFVQQTQDVRNPVIYAVFTSSGSV--FRGSAVCVYSMADIRMFVNGPFAHKE 359
Qy      359 KETSRWTTYRGPETNPRPGSCSVG---PS-----SDKALTFMKDHFMLDEQVV---GT 405
      :| : | |||:| | || | : : ||: | || : |

```

Db 360 GPNYQWMPFSGKMPYPRPGTCGGTFTPSMKSTKDYPDEVINFMRSHPLMYQAVYPLQRR 419
 Qy 406 PLLVKSGVEY--TRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVV----SGDSSAHLVEE 459
 ||::|:| | | :||: || : |::|| |:: | :| : :||
 Db 420 PLVVRTGAPYRLTTIAVDQVDSADGR-YEVFLFGTDRGTQKVIVLPKDDQEMEELMLEE 478
 Qy 460 IQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVY-ESCVDCVLARDPHCAWDP 518
 ::| || ||: : : : : :| : || : | | :| || ||||:||||
 Db 479 VEVFKDPAPVKTMTISSKRQQLYVASAVGVTHLSLHRCQAYGAACADCCCLARDPYCAWD- 537
 Qy 519 ESRTCCLLSAPN-LNSWKQDMERGNPEWACASGPMSRSLRPQSRPQIIKEV-LAVPNSIL 576
 : | :| : | :||: || | | : : :| | |
 Db 538 -GQACSRYTASSKRRSRRQDVRHGNPIRQC-----RGFNSNANKNAVESVQYGVAGSAA 590
 Qy 577 ELPCPHLSALASYW--SHGPA-----AVPEASSTVYNGSLLLIVQDGVGGLYQCWATE 628
 | | | | : | | | : | | | : | | | :| || | ||
 Db 591 FLECQPRSPQATVKWLFQRDPGDRRREIRAEDRFLRTEQGLLLRALQLSDRGLYSCTATE 650
 Qy 629 NGFSYPV--ISYWVDSQDQT-LALDPEL--AGIPREHVKVPLTRVSGGAALAAQ----- 677
 | | : | : | :| | | | : | | | | | | |
 Db 651 NNFKHVVTRVQLHVLGRDAVHAALFPPLSMSAPPPGAGPPTPPYQELAQLLAQPEVGLI 710
 Qy 678 ----QSYWPH 683
 | | |
 Db 711 HQYCQGYWRH 720

RESULT 5

A49069

collapsin - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004

C;Accession: A49069

R;Luo, Y.; Raible, D.; Raper, J.A.

Cell 75, 217-227, 1993

A;Title: Collapsin: a protein in brain that induces the collapse and paralysis of neuronal growth cones.

A;Reference number: A49069; MUID:94006554; PMID:8402908

A;Accession: A49069

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-772 <LUO>

A;Cross-references: UNIPROT:Q90607; GB:U02528; NID:g410078; PIDN:AAC59638.1;

PID:g410079

C;Superfamily: semaphorin

Query Match 20.8%; Score 838; DB 2; Length 772;

Best Local Similarity 31.6%; Pred. No. 6.4e-58;

Matches 203; Conservative 120; Mismatches 256; Indels 64; Gaps 19;

Qy 39 MPRVRYAGDERRALSFFHQKGL---QDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP 95
 :||:: : : : || : | || : : ||||:: | : : :
 Db 29 VPRCLKSYKEMLESNNIVNFNGLANSSSYHTFLLDEERSRLYVGAKDHIFSNLVN---- 84
 Qy 96 RLK--NMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTF 153
 :| | || | :| || : | :| |||:| :| |||| ||| || | ||:
 Db 85 -IKEYQKIVWPVSHSRRDECKWAGKDILRECANFIKVLKTYNQTHLYACGTGAFHPMCTY 143

Qy 154 IEL---QDSYLLPISEDKVMGKQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMR 210
 ||: : : : : |::||:| | :||| |||| :|| : : |
 Db 144 IEVGSHPEDNIFRMEDSHFENGGRGKSPYDPKLLTASLLVDGELYSCTAADFMGRDFAIFR 203

Qy 211 TLGSQPVLKTDNF--LRWLHHDASFVAA-----IPSTQVVYFFFEETASEFDDFERLHT 262
 ||| :||: ||| :| |::| | :||| | | : : :
 Db 204 TLGHHHPIRTEQHDNRWL--NDPRFISAHLPESDNPEDDKIYFFFRENAIDGEHTGKATH 262

Qy 263 SRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG----QLPFNVIRHAVLLPADSPTAP 318
 :|| :||| || : | |||||::||: || : : | : : | |
 Db 263 ARIGQICKNDFGGHRSLVNKWTTFLKARLICSVPGPNGIDTHFDELQDVFLMNSKDPKNP 322

Qy 319 HIYAVFTSQWQVGGRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPEPNRPGS 378
 :| |||: : : |||| :||: ||| | | : :| |::| ||||:
 Db 323 IVYGVFTTSSNI--FKGSAVCMYSMTDVRVFLGPYAHRDGPYQWVPYQGRVPYPRPGT 380

Qy 379 C-----SVGPSSDKALTFMKDHFLLMDEQVV---GTPLLKVGSGVEY--TRLAVETAQ 424
 | : :||: | | | :||: ||: | :||: |:
 Db 381 CPSKTFGGFDSTKDLDPDEVITFARSHPAMYNPVFPINSRPIMIKTDVDYQFTQIVVDRVD 440

Qy 425 GLDGHSHLVMYLGTGTTGSLHKAVVSGDSSAH-----LVEEIQLFDPPEPVRNLQLAPTQG 479
 || : ||::|| |:: | | : | |::: ||: | : :||: |
 Db 441 AEDG-QYDVMFIGTDIGTVLKVVSIPKETWHELEEVLLLEMTVFREPTVISAMKISTKQQ 499

Qy 480 AVFVGFSGGVWRVPRANCSVY-ESCVCVLARDPHCAWDPESTRCCLLSAPNL--NSWKQ 536
 :||: | || :|| | || :||: |||||:|||| | | : :|
 Db 500 QLYIGSATGVSQPLHRCDVYGKACAECCLARDPYCAWDGSS---CSRYFPTAKRRTRRQ 556

Qy 537 DMERGNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHG-- 594
 |: |:| |: : | : | : || | | | | ||
 Db 557 DIRNGDPLTHCSD--LQHDNPSGQTLKIIYGVENSSTFLECSPKSQRAIVYWQFQKQ 614

Qy 595 -----PAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENG 631
 | : | || :| |::| |::||
 Db 615 NDDHKVEIKVDDRMIRTEQGLLLRSLQRRDSGIYFCHAVEHGF 657

RESULT 6

I48747

semaphorin D - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I48747

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Accession: I48747

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-772 <RES>

A;Cross-references: UNIPROT:O08665; EMBL:X85993; NID:g854329; PIDN:CAA59985.1;

PID:g854330

C;Genetics:

A;Gene: semD

C;Superfamily: semaphorin

Query Match 20.7%; Score 836; DB 2; Length 772;
Best Local Similarity 30.3%; Pred. No. 9.2e-58;
Matches 220; Conservative 124; Mismatches 279; Indels 102; Gaps 25;

Qy	24	LLLPTTTAGGGGQGPMPRVRY-YAG--DERRALSFFHQKGLQDFDTLLLSGDGNTLYVGA	80
		: : : : : : : : :	
Db	14	VLLTARANYANGKNNVPRKLKSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGA	73
Qy	81	REAILALDIQDPGVPRLKNM--IPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTH	138
		:: : :: : : : : : : : : :	
Db	74	KDHIFSFNLVN-----IKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLEAYNQTH	128
Qy	139	LYTCGTFAFSPACTFIEL---QDSYLLPISEDKVMGKGQSPFDPAHKHTAVLVDGMLYS	195
		: : : : : : : : : : :	
Db	129	LYACGTGAFHPICTYIEVGHPEDNIFKLQDSHFENGGRGKSPYDPKLLTASLLIDGELYS	188
Qy	196	GTMNNFLGSEPIILMRTLGSQPVLKTDNF-LRWLHHDASFVAA-----IPSTQVVYFFF	247
		: : : : : : :	
Db	189	GTAADFMRDFAIFRTLGDHHPIRTEQHDNRWL-NDPRFISAHLPESDNPEDDKVYFFF	247
Qy	248	EETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG----QLPFNV	303
		: : : : : : : :	
Db	248	RENAIGGEHSGKATHARIGQICKNDFGGHRSVLNKWTTFLKARLICSVPGPNGIDTHFDE	307
Qy	304	IRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSR	363
		: : : : : : : : : : : : :	
Db	308	LQDVFLMNSKDPKNPIVYGVFTTSSNI--FKGSAVCMYSMSDVRVFLGPYAHRDGPNYQ	365
Qy	364	WTTYRGPETNPRPGSC-----SVGPSSDKALTFMKDHFMLDEQVV---GTPLL VKS	411
		: : : : : : :	
Db	366	WVPYQGRVPYPRPGTCPSKTFGGFDSTKDLRDDVITFGRSHPAMYNPVFPINNRPIMIKT	425
Qy	412	GVEY---TRLAVETAQGLDGSHLVMYLGTTTGSLHKAVVSGDSSAH-----LVEEIQLFP	464
		: : : : : : : : :	
Db	426	DVNYQFTQIVVDRVDAEDG-QYDVMFIGTDVGTVLKVVSVPKETWHDLEEVLLEEMTVFR	484
Qy	465	DPEPVRNLQLAPTQGAVFVGFGSGGVWRVPRANCSVY-ESCVDCVLARDPHCAWD PESRTC	523
		: : : : : : : : : :	
Db	485	EPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAWDGSS---	541
Qy	524	CLLSAPNL--NSWKQDMERGNPEWACAS-----GPMRSRLRPQSRPQIIKEVLAVPN	573
		: : : : : : :	
Db	542	CSRYFPTAKRRTRRRQDIRNGDPLTHCSDLHDHNNHGP---SLEE-----RIIYGVEN	591
Qy	574	SILELPCPHLSALASYW-----SHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCW	625
		: : :	
Db	592	SSTFLECSPKSQRALVYWQFQRRNRRSKREIRMGDHIIRTEQGLLLRSLQKKDSGNYLCH	651
Qy	626	ATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGG-----AALAA	676
		: : : : :	
Db	652	AVEHGFM-----QTL-LKVTLEVIDTEHLEELLHKDDDGDSKIKEMSSSMTTP	698
Qy	677	QQSYW 681	
Db	699	SQKVW 703	

RESULT 7

D49423

semaphorin III precursor - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: D49423

R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules.

A;Reference number: A49423; MUID:94094332; PMID:8269517

A;Accession: D49423

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-771 <KOL>

A;Cross-references: UNIPROT:Q14563; GB:L26081; NID:g799328; PIDN:AAA65938.1; PID:g436560

C;Genetics:

A;Gene: GDB:SEMA1

A;Cross-references: GDB:283448

C;Superfamily: semaphorin

Query Match 20.5%; Score 825.5; DB 2; Length 771;
Best Local Similarity 30.5%; Pred. No. 6.2e-57;
Matches 216; Conservative 119; Mismatches 282; Indels 91; Gaps 24;

Qy 35 GQGPMPRVRY-YAG--DERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQD 91
|: :||:: | : ::| : | | : : ||||:: | : |: :
Db 25 GKNVPRKLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHI FSFDLVN 84

Qy 92 PGVPRLKNM--IPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSP 149
:|: | | | : : | | : | : | | | : | | | | | | | |
Db 85 -----IKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGAFHP 139

Qy 150 ACTFIEL---QDSYLLPISEDKVMGKGQSPFDPAHKHTAVLVDGMLYSGTMNIFLGSEP 206
||:|: : : : |:|:|:| : :|:| | | | :|:| :
Db 140 ICTYIEIGHHPEDNIFKLENSHFENGGRKSPYDPKLLTASLLIDGELYSGTAADFMGRDF 199

Qy 207 ILMRTLGSQPVLKTDNF-LRWLHHDASFVAA-----IPSTQVVYFFFEETASEFDFFE 258
: | | | : :|: | | :| |:| | | | | | : :
Db 200 AIFRTLGHHPHPIRTEQHDSRWL-NDPKFISAHLISESDNPEDDKVYFFFRENAIDGEHSG 258

Qy 259 RLHTRSARVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG----QLPFNVIRHAVLLPADS 314
: :|: :||| | | : | | | | | | :|: | | | : : | :
Db 259 KATHARIGQICKNDFGGHRSLVNKWTTFLKARLICSVPGPNGIDTHFDELQDVFLMNFKD 318

Qy 315 PTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNP 374
| | :| | | : : : | | | :|: | : | | | : :| | :| |
Db 319 PKNPVVYGVFTTSSNI--FKGSAVCMYSMSDVRVFLGPYAHRDGPYQWVPYQGRVPYP 376

Qy 375 RPGSC-----SVGPSSDKALTFMKDHFLLMDEQVV---GTPLLKSGVEY--TRLAV 420
||:| | | :|: | :| | | | | | : :|: | | | :|: |
Db 377 RPGTCPSKTFGGFDSTKDLPPDVITFARSHPAMYNPVFPMNNRPVIVIKTDVNYQFTQIVV 436

Qy 421 ETAQGLDGHSHLVMYLGTGTTGSLHKAV-----VSGDSSAHLVEEIQLFPDPEPVRNLQLA 475

```

      :   || : ||::|| |:: | |   |   |::||: :| :| : :||:
Db      437 DRVDAEDG-QYDVMFIGTDVGTVLKVVSIPKETWYDLEEVLLLEEMTVFREPTAISAMELS 495

Qy      476 PTQGAVFVGFSGGVWRVPRANCSVY-ESCVDCVLARDPHCAWDPESTRCCLLSAPNL--N 532
      | :::| : || ::| | :| ::| :| ||||:|||| : | |
Db      496 TKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAWD---GSACSRYFPTAKRR 552

Qy      533 SWKQDMERGNPEWACAS--GPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASY 590
      : :||: |::| |: |::| |: | | | | | | | | | |
Db      553 TRRQDIRNGDPLTHCSDLHHDNHHGHSPEER-----IIYGVENSSTFLECSPKSQRALVY 607

Qy      591 WS-----HGPAAVPEASSTVYNGSLLLVQDGVGGLYQCWATENGFSYPVISYWVDS 642
      |   |   | :   | || :|   | | | | |::|
Db      608 WQFQRRNEERKEEIRVDDHIIRTDQGLLLRSLQKDSGNYLCHAVEHGF----- 657

Qy      643 QDQTLALDPELAGIPREHVKVPLTRVSGG-----AALAAQQSYW 681
      ||| | | | ||:: | : |   : : | |
Db      658 --QTL-LKVTLEVIDTEHLEELLHKDDGDGSKTKEMSNSMTPSQKVW 702

```

RESULT 8

G01856

semaphorin V - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C;Accession: G01856

R;Sekido, Y.

submitted to the EMBL Data Library, June 1995

A;Reference number: G08634

A;Accession: G01856

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-749 <SEK>

A;Cross-references: UNIPROT:Q13214; EMBL:U28369; NID:g974283; PIDN:AAD09138.1;

PID:g974284

C;Superfamily: semaphorin

Query Match 20.3%; Score 820; DB 2; Length 749;

Best Local Similarity 31.2%; Pred. No. 1.6e-56;

Matches 207; Conservative 116; Mismatches 254; Indels 86; Gaps 24;

```

Qy      32 GGGGQGPMPRVRYAGDERRALSF-----FHQKGLQDF-----DTLLSGDGNTLYV 78
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      20 GLGSAAPSP-----PRLRSLFQELQAWH--GLQTFSLERTCCYQALLVDEERGRLFV 69

Qy      79 GAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTH 138
      || : :||: : : : : : ||| : || : | |::| :|| |
Db      70 GAENHVASLNLDN--ISKRAKLAWPAPVEWREECNWAGKDIGTECMNFVKLLHAYNRTH 127

Qy      139 LYTCGTFAFSPACTFIEL---QDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYS 195
      | ||| || | | |:: : : : : : ||| : || : | |::| :|| |
Db      128 LLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGRIEDGKGKSPYDPRHRAASVLVGEELYS 187

Qy      196 GTMNNFLGSEPILMRTLGSQPVLKTD-NFLRWLHHDASFVAI-----PSTQVVYFFF 247
      | : :| : : |::| : |::: : ||| : : | | : |||
Db      188 GVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWL-NEPKFVKVFWIPESENPDDDKIYFFF 246

```

Qy 248 EETASE-FDFFERLHTSRVARVCKNDVGGKLLQKKWTTFLKAQLLCTQP---GQLPFNV 303
 ||| | || ||| ::|:|||||:: | ||||| |:|: | | |:
 Db 247 RETAVEAAPALGRLSVSRVGQICRNDVGGQSRSLVNKWTTFLLKARLVCSVPGVEGDTHFDQ 306

Qy 304 IRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSR 363
 :: || : | :|||:: : : ||| |:|: | | | : :
 Db 307 LQDVFLSSRDHRTPLLYAVFSTSSSI--FQGSACVYSMNDVRRRAFLGPFAPFAHKEGPMHQ 364

Qy 364 WTTYRGPETNPRPGSC-----SVGPSSDKALTFMKDHFMLDEQV---GTPLL VKS 411
 | :|:| ||| | | : | :| || | : | || :
 Db 365 WVS YQGRVPYPRPGMCPSKTFGTFSSTKDFDDVIQFARNHPLMYNSVLPTGGRPLFLQV 424

Qy 412 GVEY--TRLAVETAQGLDGSHLVMYLGTTTGSLHK--AVVSG---DSSAHLVEEIQ LFP 464
 | | | :| : || : | : :|| | : | : | : | :| :| :
 Db 425 GANYTFTQIAADRVAADGH-YDVLFIGTDVGTVLKVISVPKGSRPSAEGLLLEELHVFE 483

Qy 465 DPEPVRNLQLAPTQGA VFGVSGGVWRVPRANCSVY-ESCVD CVLARDPHCAWD PESRTC 523
 | | :| : : : :| | : : | : | ||||| :|||
 Db 484 DSAAVTSMQISSKRHQLYVASRSAVAQIALHRCAAHGRVCTECCLARDPYCAWD---GVA 540

Qy 524 CLLSAPNLNS--WKQDMERGNPEWACASGPM SRSRLRPQSRPQIIK-EVLAVPNSILELPC 580
 | | : :||: | :| | : ||| :: : | | | | |
 Db 541 CTRFQPSAKRRFRQQDVRNGDPSTLCSG-----DSSRPALLEHKVFGVEGSSAFLEC 592

Qy 581 PHL SALASYW-----SHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENGFS 632
 | | | :| | : | || : | :| | | ||:
 Db 593 EPRSLQARVEWTFQ RAGVTAHTQVLAEERTERTARGLLLRRLRRRDSGVYLC AAVEQGF 652

Qy 633 YPV 635
 |:
 Db 653 QPL 655

RESULT 9

I48748

semaphorin E - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I48748

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin.D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Accession: I48748

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-751 <RES>

A;Cross-references: UNIPROT:Q62181; EMBL:X85994; NID:g854331; PIDN:CAA59986.1; PID:g854332

C;Genetics:

A;Gene: semE

C;Superfamily: semaphorin

Query Match 19.9%; Score 802.5; DB 2; Length 751;
 Best Local Similarity 31.2%; Pred. No. 4e-55;
 Matches 219; Conservative 119; Mismatches 264; Indels 101; Gaps 26;

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Accession: I48744

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-748 <RES>

A;Cross-references: UNIPROT:Q62177; EMBL:X85990; NID:g854323; PIDN:CAA59982.1; PID:g854324

C;Genetics:

A;Gene: semA

C;Superfamily: semaphorin

Query Match 19.5%; Score 784.5; DB 2; Length 748;
Best Local Similarity 31.1%; Pred. No. 1e-53;
Matches 210; Conservative 117; Mismatches 281; Indels 67; Gaps 23;

```
Qy      31 AGGGGQGP-MPRVR--YYAGDERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILAL 87
      || | | :||:| : | : | : : ||: : |:||| : :|
Db      19 AGLGDTAPNLPRLRLSFQELQARHGVRTFRLEERTCCYEALLVDEERGRLFVGAENHVASL 78

Qy      88 DIQDPGVPRCLKNMIWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAF 147
      : : : : : ||| : || : | | :| ||:|:| :|| ||| | |||
Db      79 SLDN--ISKRAKKLAWPAPVEWREECNWAGKDIGTECMNFVRLHAYNHTHLLACRTGAF 136

Qy     148 SPACTFIELQDSYLLPIS--EDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNFFLGSE 205
      | | : | : | :||:|:|:|:| | : ||| ||| : :| :
Db     137 HPTCALWRWATAGGTHASTGPEKLEDGKGKTPYDPRHRPPSVLVGEELYSGVTADLMGRD 196

Qy     206 PILMRTLGSQPVLKTD-NFLRWLHHDASFVAI-----PSTQVVYFFFEETASE-FDF 256
      : |:|| | | :|: : ||| :: || | : |||| | :| |
Db     197 FTIFRSLGQNPSLRTEPHDSRWL-NEPKFVKVFWIPESENPDDDKIYFFRFRESAVEAAPA 255

Qy     257 FERLHTSRVARVCKNDVVGGEKLLQKKWTTFLKAQLLCTQP---GQLPFNVIRHAVLLPAD 313
      |: ||| ::|:|:|:|:| | | ||||| |:|:| | | | : : || :
Db     256 MGRMSVSRVQGICRNDLGGQSRSLVNKWTTFLKARLVCSVPGVEGDTHFDQLQDVFLSSR 315

Qy     314 SPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETN 373
      | :|||: : | : ||| :|: | : | | | | : | :|:|
Db     316 DRQTPLLYAVFST--SSGVFQGSAVCVYSMNDVRR AFLGPLPHKEGPTHQWVS YQGRVPY 373

Qy     374 PRPGSC-----SVGPSSDKALTFMKDHFMDQV---GTPLLVKSGVEY--TRLA 419
      |||| | | : | :|:| || | : | || : : | | | :|
Db     374 PRPGMCPSKTFGTFSSTKDFPDDVIQFGRNHPLMYPVLP MGG RPLFLQVGAGYTFTQIA 433

Qy     420 VETAQGLDGHSHLVMYLGT T T T G S L H K --AVVSG---DSSAHLVEEIQLFPDPEPVRNLQL 474
      : ||| : |:::| | :| : | : | :| :|:|:| | : : :|:
Db     434 ADRVAAADGH-YDVLFIGTDVGTVLKVISVPKGRRPNSEGLLLEELQVFEDSAAITSMQI 492

Qy     475 APTQGAVFVGFGSGGVWRVPRANCSVY-ESCVCVLARDPHCAWDPE SRTCCLLSAPNLNS 533
      : : : :| | : : | : :| :| ||||:| || : | |
Db     493 SSKRQQLYVASRAAVAQIALHRCTALGRACAECCLARDPYCAWD---GSACTRFQPTAKR 549

Qy     534 --WKQDMERGNPEWACASGPM S R L R P Q S R P Q I I K E V L A V P N S I L E L P C P H L S A L A S Y Y W 591
      :||: | :| | || | | : : | :| | : | | | |
Db     550 RFRRQDIRNGDPSTLC-SGDSSHSV-----LLEKKVLGVESGSAFLECEPRSLQAHVQW 602
```

```

Qy      592 -----SHGPAAVPEASSTVYNGSLLLLIVQDGVGGLYQCWATENGFSYP----VISYW 639
           :|          |          ||  ::  |:| | | | || |  |:
Db      603 TFQGAGEAAHTQVLAEEVERTARGLLLRGLRRQDSGVYLCVAVEQGFSQPLRRLVLHVL 662

Qy      640 VDSQDQTLALDPELA 654
           :| : ||  | |
Db      663 SAAQAERLARAEAAA 677

```

T58169

semaphorin III - mouse (fragment)

C;Species: Mus musculus (house mouse)

C:\Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text change 09-Jul-2004

C;Accession: I58169

R;Messersmith, E.K.; Leonardo, E.D.; Shatz, C.J.; Tessier-Lavigne, M.; Goodman, C.S.; Kolodkin, A.L.

Neuron 14, 949-959, 1995

A;Title: Semaphorin III can function as a selective chemorepellent to pattern sensory projections in the spinal cord.

A;Reference number: I58169; MUID:95267432; PMID:7748562

A;Accession: I58169

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-666 <RES>

A;Cross-references: UNIPROT:O08665; GB:L40484; NID:g703189; PIDN:AAA73934.1;
PID:g703190

C;Genetics:

A; Gene: SemaIII

C;Superfamily: semaphorin

Query Match 19.0%; Score 766; DB 2; Length 666;

Best Local Similarity 31.4%; Pred. No. 2.6e-52;

Matches 195; Conservative 102; Mismatches 232; Indels 92; Gaps 21;

QY 123 QCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIEL---QDSYLLLPISDKVMGKQSPFD 179
:| |||:| | ||| || | ||:| : : : |::|:|
Db 7 ECANFIKVL EAYNOTHLYACGTGAFHPICTYIEVGHHPEDNIFKLQDSHFENGGRGKSPYD 66

QY 180 PAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNF-LRWLHHDDASFVAA-- 236
| ::||| |||| ||: : : |||| ::| ||| :| |:|
Db 67 PKLLTASLLIDGELYSGTAANFMGRDFAIFRTLGHHPPIRTEQHDRWL-NDPRFISAHL 125

QY 237 -----IPSTQVVFYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQL 291
| | | | | | : : : : | | : | | | | | : |
Db 126 IPESDNPEDDKVYFFFRENAIDGEHSGKATHARIGQICKNDFGGHRSLVNKWTTFLKARL 185

QY 292 LCTQPG----QLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIE 347
:|: || |:: |: : | |: | ||: : : ||| :|: |:

Db 186 ICSVPGPNGIDTFEDELQDVFLMNSKDPKNPIVYGVFTTSSNI--FKGSAVCMYSMSDVR 243

Qy 348 RVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDKALTFMKDHFLLM 398
|| | | : :| |:| |||:| | | :|| : | |
Db 244 RVLGLPYAHRDGPNYOWVPYOGRPYPRPGTCPSKTEGGFDSTKDLPPDVITFARSHPM 303

Qv 399 DEQVV---GTPLLVKSGVEY--TRLAVETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSS 453


```

      |      |::|: | | |:: |:      || : ||::|| |:: | |      :
Db      304 YNPVFPINNRPIMIKTDVNYQFTQIVVDRVDAEDG-QYDVMFIGTDVGTVLKVVSVPKET 362
Qy      454 AH-----LVEEIQLFDPDEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVY-ESCVDCV 507
      |      |::|: | | |: |: |: | |::| | |: | | |: | | |: | |
Db      363 WHDLEEVLLLEMTVFREPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECC 422
Qy      508 LARDPHCAWDPESTRCCLLSAPNL--NSWKQDMERGNPEWACAS-----GPMRSRLR 557
      |||||:|||| | | | : ||: |:: |: | | | | | |
Db      423 LARDPYCAWDGSS---CSRYFPTAKRRTRRRQDIRNGDPLTHCSDLQHHDNHGHP---SLE 476
Qy      558 PQSRPQIIKEVLAVPNSILELPCPHLSALASYYS-----HGPAAVPEASSTVYNGS 609
      : : | || | | | | | | | | | | | | | | | | | | | | |
Db      477 E-----RIIYGVENSTFLECSPKSQRALVYWQFQRNEDRKEEIKMGDHIIRTEQGL 529
Qy      610 LLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPPLTRVS 669
      || :| | | | |::|| | | | | | | | | | | | | | | | |
Db      530 LLRSIQKKDSGNYLCHAVEHGFM-----QTL-LKVTLEVIDTEHLEELLHKDD 576
Qy      670 GG-----AALAAQQSYW 681
      |      :: | |
Db      577 DGDGSKIEMSSSMTPSQKVW 597

```

RESULT 12

JC5928

semaphorin F precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: JC5928

R;Simmons, A.D.; Pueschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M.
Biochem. Biophys. Res. Commun. 242, 685-691, 1998

A;Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-
chat candidate interval.

A;Reference number: JC5928; MUID:98125554; PMID:9464278

A;Accession: JC5928

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1074 <SIM>

A;Cross-references: UNIPROT:Q13591; GB:U52840; NID:g2772583; PIDN:AAC09473.1;
PID:g2772584

A;Experimental source: brain

C;Comment: This protein disrupts normal brain development and leads to some of
the features of Cri-du-chat.

C;Genetics:

A;Gene: semaF

C;Superfamily: human semaphorin F; thrombospondin type 1 repeat homology

F;1-20/Domain: signal sequence #status predicted <SIG>

F;50-533/Domain: semaphorin #status predicted <SEM>

F;840-896/Domain: thrombospondin type 1 repeat homology <THR3>

F;971-993/Domain: transmembrane #status predicted <TMM>

Query Match 16.8%; Score 677.5; DB 2; Length 1074;

Best Local Similarity 34.1%; Pred. No. 5.3e-45;

Matches 170; Conservative 87; Mismatches 207; Indels 35; Gaps 18;

Qy 56 FHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLLKNMIPWPASDRKKSECAF 115

Db	50	FRAKNAADFSQLTFDPGQKELVVGARNYLFRLQLEDLS---LIQAVEWECDEATKKACYS	106
Qy	116	KKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGGQ	175
Db	107	KGKSKE-ECQNYIRVLL-VGGDRLFTCGTNAFTPVCTNRSL--SNLAEIHDQ--ISGMAR	160
Qy	176	SPFDPAHKHTAVL-VDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNF-LRWLHHDAF	233
Db	161	CPYSPQHNSTALLTAGGELYAATAMDFPRDPAIYRSLGILPPLRTAQYNSKWL-NEPNF	219
Qy	234	VAAIPSTQVVYFFFEETASEFDFFERLHTRSARVAVCKNDVGGEKLLQKKWTTFLKAQLLC	293
Db	220	VSSYDIGNFTYFFFRENAVEHDCGKTVF-SRAARVCKNDIGGRFLEDWTWTFMKARLNC	278
Qy	294	TQPGQLPF--NVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFK	351
Db	279	SRPGEVPFYYNELQSTFFL----PELDLIYGIFTT--NVNSIAASAVCVFNLSAIAQAFS	332
Qy	352	GKYKELNKETSRWTTYRGPETNPRPGSCSVG-----PSSDKALTFMKDHFLMDEQVVG	404
Db	333	GPFKYQENSRSAWLPYPNPNPHFQCGTVDQGLYVNLTERNLQDAQKFILVHEVV-QPVT	391
Qy	405	TPLLKSGVEYTRLAVETAQGLDGHSHLVMYLGTTTGSLSHKAVV--SGDSSAHLVEEIQ	462
Db	392	VPSFMEDNSRFESHVAVDVVQGREALVHII-YLATDYGTIKKVRVPLNQTSSSCLLEEIE	450
Qy	463	FPD--PEPVRNLQLAPTQGAFFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE	520
Db	451	FPERRREPIRSLQILHSQSVLFVGLREHVVKIPLKRCQFYRTRSTCIGAQDPYCGWDV	510
Qy	521	RTCCLL-SAPNLNSWKQDM	538
Db	511	KKCTSLEESLSMTQWEQSI	529

RESULT 13

JH0798

fasciclin IV precursor - American bird grasshopper

C;Species: Schistocerca americana (American bird grasshopper)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: JH0798

R;Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Goodman, C.S.

Neuron 9, 831-845, 1992

A;Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in the grasshopper embryo.

A;Reference number: JH0798; MUID:93040225; PMID:1418998

A;Accession: JH0798

A;Molecule type: mRNA

A;Residues: 1-730 <KOL>

A;Cross-references: UNIPROT:Q26473; GB:L00709; NID:g160844; PID:g160845

A;Experimental source: embryo

C;Comment: This protein plays a role in growth cone guidance in the developing central nervous system.

C;Keywords: glycoprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-730/Product: fasciclin IV #status predicted <MAT>
 F;23-627/Domain: extracellular #status predicted <EXT>
 F;628-652/Domain: transmembrane #status predicted <TMM>
 F;653-730/Domain: intracellular #status predicted <INT>
 F;44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.3%; Score 657.5; DB 2; Length 730;
 Best Local Similarity 29.5%; Pred. No. 1.1e-43;
 Matches 213; Conservative 115; Mismatches 246; Indels 149; Gaps 34;

Qy	41	RVRYAGDERRALSFFHQGLQDFDTLLSGDGNTRYVGAREAILALDIQDPGVPRLKNM	100
		: : : : : : : :	
Db	37	RVQRFLGNESHKDH-----KLEKDHNSLLVGARNIVYNISLRDL-TEFTEQR	84
Qy	101	IPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQD-S	159
		: : : : : : :	
Db	85	IEWHSSGAHRELCYLKGS-EDDCQNYIRVLAKIDDDRVLICGTNAYKPLCRHYALKDGD	143
Qy	160	YLLPISEDKVMEGKGQSPFDPAHKHATAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLK	219
		:: : : : : : : ::: :	
Db	144	YVV----EKEYEGRGLCPFDPDHNSTAIYSEGQLYSATVADFSGTDPLIYR----GPLRT	195
Qy	220	TDNFLRWLHHDAFVAAPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLL	279
		: : : : : : : : :	
Db	196	ERSDLKQL-NAPNFVNTMEYNDFIFFFFRETAVEYINCGKAIYSRVARVCKHDKGGPHQF	254
Qy	280	QKKWTTFLKAQLLCTQPQGQLP--FNVIRHAVLLPAD-----SPTAPHIYAVFTSQWQV	330
		: : : : : : : :	
Db	255	GDRWTSFLKSRLNCSVPGDYPFYFNEIQST----SDIEGNYGGQVEKLIYGVFTT--PV	308
Qy	331	GGTRSSAVCAFSLLDIERVFKGKYKELNKETSrw---TTYRGPETNPRPGSCSVGPS---	384
		: : : :	
Db	309	NSIGGSAVCAFSMKSILESFDGPFKEQETMNSNWLAVPSLVPE--PRPGQC-VNDSRTL	365
Qy	385	SDKALTfMKDHFfLMDEQVVG---TPLLVKSGVEY--TRLAV-ETAQGLDGHSHLVMYLGT	438
		:: : : : : : : : :: : :	
Db	366	PDVSVNFVKSHTLMDAEPAFFTRPILIRISLQYRFTKIAVDQQVRTPDGKAYDVLFIGT	425
Qy	439	TTGSLHKAV--VSGDSS----AHLVEEIQLFDPPEPVRNLQLAPTQG--AVFVGfSGG--	488
		: : : : : : : :	
Db	426	DDGKVIKALNSASFSSDTVDVSVIEELQVLPPGVPVKNLYVVRMDGDDSKLVVSDDEI	485
Qy	489	-VWRVPRANCSVYESCVDCVLARDPHCAWDPEsrTCCLLSAPNLNSWK-----QDMERGNP	543
		:: : : : : : : : : ::	
Db	486	LAIKLHRCGSDKITNCRECVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEH	545
Qy	544	EWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASS	603
		: : : :	
Db	546	K-ACGG-----RPQT-----EIVASP-----VPTQPT	566
Qy	604	TVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPEL-----AGIPR	658
		: : : : :	
Db	567	TKSSG-----DPVHSIHQA-----EFEPEIDNEIVIGVDD	596
Qy	659	EHVKVPLTRVS---GGAALAAQQSYWPHFVTVTVLFALVLS--GALII-LVASPLRALRA	712
		: : : : : : : : :	


```

Db      342 GRFKEQKTPDSVWTAV--PEDKVPKPRPGCCAKHGLAEAYKTSIDFPDDTLAFIKSHPLM 399
Qy      399 DEQV---VGTPLLVKSGVEYTRLAVETAQGLDGH-SHLMYLGTTTGSLLHKAVVSGD--- 451
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      400 DSAVPPIADEPWFTKTRVRYRLTAIEVDRSAGPYQNYTVIFVGSEAGVVLKVLAKTSPFS 459
Qy      452 -SSAHLVEEIQLF-----PDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANC SVYE 501
      : : | : | | : : : : | : | | : : | : | | : : | : | |
Db      460 LNDVLLLEEIEAYNPAKCSAESEEDRKVVSLLQDKDHHALYVAFSSCVVRIPLSRCERYG 519
Qy      502 SC-VDCVLARDPHCAWDPESTRCC-----LLSAPNL-----NSWKQDMERGNP-- 543
      || | : : | | : | | : | | : | | : | | : | | : | |
Db      520 SCKKSCIASRDPYCGW--LSQGVCEVTLGMLLLTEDFFAFHNHSPGGYEQDTEYGNTAH 577
Qy      544 -----EWACASGPMRSRLRQSRPQIIKEVLAVPNSILELPC-----PHLSALAS 588
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      578 LGDCHGVRWEVQSG-----ESNQMVHNMVL-----ITCVFAAFVLGAFIAGVAV 621
Qy      589 YYWS-----HGPAAVPEASSTVYNGSLLLVQDGVGGGLYQCWATENG-FSYPVIS 637
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      622 YCYRDMFVRKNRKIKDAESAQ-SCTDSSGS-----FAKLNGLFDSPVKE 665
Qy      638 YW--VDS-----QDQTLALD-----PELAGIP 657
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      666 YQQNIDSPKLYSNLLTSRKELPPNTDTKSMVADHRGQPPELAALP 710

```

RESULT 15

T27165

hypothetical protein Y54E5B.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T27165

R;Lennard, N.

submitted to the EMBL Data Library, October 1998

A;Reference number: Z20321

A;Accession: T27165

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-712 <WIL>

A;Cross-references: UNIPROT:Q17330; EMBL:AL032653; PIDN:CAA21714.1;

GSPDB:GN00019; CESP:Y54E5B.1

A;Experimental source: clone Y54E5B

C;Genetics:

A;Gene: CESP:Y54E5B.1

A;Map position: 1

A;Introns: 36/1; 70/2; 85/3; 194/2; 221/1; 253/3; 301/1; 352/3; 522/2; 560/1; 599/3; 655/3

```

Query Match      15.4%; Score 621.5; DB 2; Length 712;
Best Local Similarity 31.1%; Pred. No. 7.8e-41;
Matches 196; Conservative 97; Mismatches 233; Indels 105; Gaps 29;

```

```

Qy      68 LLSGDGNTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKSNETQCFNF 127
      ||: ||: || || | | : | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      57 LLAADGDSLLVGARNVYNLSLSTLSV---NHKIDWKPPAEHIEECIMKGKS-KTDCQNY 112

```

Qy 128 IRVLVSYNVTHLYTCGTFASFPACTFIELQDSYLLPISEDKVMGKQSPFDPAHKHTAV 187
 |||| : ||| |||| | : : | : :|| ||:| | :|:
 Db 113 IRVLARKSAGVSLVCGTHAFSPKCREYTVTE---FGIRNTRQFDGQGISPYDPKHNSAL 169

Qy 188 LVDG--MLYSGTMNNFLGSEPILMR-TLGSQPVLKTDNFLRWLHHDA-----SFVAAIP 238
 | | | : | : :|:|: : : | | : | | : :| :|| :|||
 Db 170 YVPGTNQLFVATVTD FVGNDALIYRKTIDETPSSKSAANIRTQSYDARVLNAPNFVATFA 229

Qy 239 STQVVYFFFEETASE-FDFFERLHT-SRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQP 296
 : |||:| | ||| | | :||| |||| | | : :||:| ||:| | :|
 Db 230 YKEHVYFWFREIASEAIDNNEEPQIYARVARVCKNDKGGARPANERWTSYLKARLNCSLP 289

Qy 297 -GQLP--FNVIRHAVLLPADSPTAPH-IYAVFTSQWQVGGTRSSAVCAFSLLDIERVF-K 351
 | | || :| || | | : | :| ||:| | |||| | : | |
 Db 290 SGSSPFYFNELK-AVSDPIDAGNNNHVVYTVFST--PDSDVMSAVCKFSMKKIREEFDN 346

Qy 352 GKYKELNKETSRWTTY-RGPETNPRPGSCSVGPSSDK----ALTFMKDHFMLDEQV--VG 404
 | :| | | | : | ||||| | | | :|:| | | : |
 Db 347 GTFKHQNAQSMWMAFNREVPKPRPGSCS--PDSTKLPENTVVSFILHHPLLRPIPSVA 404

Qy 405 TPLLVKSG--VEYTRLAV-ETAQGLDGSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQ 461
 ||||: : | :| : : ||: : :||: | : | || | :| : :
 Db 405 APLLVEGADRADLTQITVLPVRVAVGGHNYDILFIGTSDGKVLK-VVEVDGNATVIQSAT 463

Qy 462 LFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWD PESR 521
 :| | :| | | : :| : : : :| ||: || || :||| |||
 Db 464 VFQRGVPIVN--LLTTKESVVI VSADEIASLPVHNCAQQTSCSKCVQLQDPHCAWDSSIA 521

Qy 522 TCCLLSAPNLNSWK-----QDMERGNPEWACASG-----PMSRSLRPQ 559
 | : || | :| | | | | :||| | :
 Db 522 RCV-----HGGSWTGDQFIQNMVFGQSE-QCPEGIIVREVFD DNESEAQPEAVSRSGYPK 575

Qy 560 SRPQIIKEVLAVPNSILELPC-----PHLSALA---SYWWSHGPA--- 597
 | :| | :| | || || : | | | | |
 Db 576 EHSTITVVLVA AVASLISLIIGAFIGIRVNRWAATSEPHRSASSTSGSDYDSFGRARLTR 635

Qy 598 -----VPEASSTVYNGSLLLIV 614
 ||: :| ||: :
 Db 636 HDSLTTATKVDHGFVPQSKQSV DATSLVMSI 666

Search completed: February 10, 2005, 02:19:23
 Job time : 65 secs

OM protein - protein search, using sw model

Run on: February 10, 2005, 02:08:03 ; Search time 138 Seconds
(without alignments)
1796.084 Million cell updates/sec

Title: US-10-015-391A-277

Perfect score: 4031

Sequence: 1 MALPALGLDPWSLLGLFLFQ.....CRTSASDVADANNCLGTEVA 761

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4031	100.0	761	10	US-09-759-130B-389	Sequence 389, App
3	4031	100.0	761	13	US-10-042-431-19	Sequence 19, Appl
39	4031	100.0	761	14	US-10-013-909A-277	Sequence 277, App
67	4031	100.0	761	15	US-10-401-053A-2	Sequence 2, Appli
69	4031	100.0	761	16	US-10-741-790-389	Sequence 389, App
70	3997	99.2	754	15	US-10-190-115-10	Sequence 10, Appl
71	3997	99.2	754	15	US-10-369-072-10	Sequence 10, Appl
72	3980	98.7	761	14	US-10-050-882-51	Sequence 51, Appl
73	3966.5	98.4	756	15	US-10-190-115-8	Sequence 8, Appli
74	3966.5	98.4	756	15	US-10-369-072-8	Sequence 8, Appli
75	3875	96.1	730	10	US-09-759-130B-391	Sequence 391, App
76	3875	96.1	730	13	US-10-042-431-21	Sequence 21, Appl
77	3875	96.1	730	16	US-10-741-790-391	Sequence 391, App
78	3847.5	95.4	730	15	US-10-470-360-11	Sequence 11, Appl
79	3810.5	94.5	762	15	US-10-190-115-35	Sequence 35, Appl
80	3810.5	94.5	762	15	US-10-369-072-35	Sequence 35, Appl
81	3761.5	93.3	742	15	US-10-401-053A-1	Sequence 1, Appli
82	3486	86.5	652	10	US-09-759-130B-392	Sequence 392, App
83	3486	86.5	652	13	US-10-042-431-22	Sequence 22, Appl
84	3486	86.5	652	16	US-10-741-790-392	Sequence 392, App
85	3300.5	81.9	629	15	US-10-104-047-2289	Sequence 2289, Ap
86	3280.5	81.4	760	10	US-09-759-130B-440	Sequence 440, App
87	3280.5	81.4	760	10	US-09-759-130B-446	Sequence 446, App
88	3280.5	81.4	760	13	US-10-042-431-70	Sequence 70, Appl
89	3280.5	81.4	760	13	US-10-042-431-76	Sequence 76, Appl
90	3280.5	81.4	760	15	US-10-190-115-36	Sequence 36, Appl
91	3280.5	81.4	760	15	US-10-369-072-36	Sequence 36, Appl
92	3280.5	81.4	760	15	US-10-401-053A-4	Sequence 4, Appli
93	3280.5	81.4	760	16	US-10-741-790-440	Sequence 440, App
94	3280.5	81.4	760	16	US-10-741-790-446	Sequence 446, App
95	2968.5	73.6	675	15	US-10-401-053A-3	Sequence 3, Appli
96	1743	43.2	328	15	US-10-190-115-37	Sequence 37, Appl
97	1743	43.2	328	15	US-10-369-072-37	Sequence 37, Appl
577	1274	31.6	837	14	US-10-241-220-57	Sequence 57, Appl
594	1274	31.6	837	14	US-10-174-587-454	Sequence 454, App
634	1274	31.6	837	14	US-10-013-909A-253	Sequence 253, App
654	1274	31.6	837	15	US-10-170-385-91	Sequence 91, Appl
674	1274	31.6	837	15	US-10-295-027-193	Sequence 193, App
675	1274	31.6	837	15	US-10-295-027-1211	Sequence 1211, Ap
686	1274	31.6	837	15	US-10-188-832-206	Sequence 206, App
688	1274	31.6	893	9	US-09-908-193-45	Sequence 45, Appl
689	1274	31.6	893	15	US-10-190-115-38	Sequence 38, Appl
690	1274	31.6	893	15	US-10-369-072-38	Sequence 38, Appl
691	1271.5	31.5	832	11	US-09-833-245-1271	Sequence 1271, Ap
692	1239	30.7	791	9	US-09-908-193-18	Sequence 18, Appl
693	1198.5	29.7	782	9	US-09-908-193-47	Sequence 47, Appl
694	1198.5	29.7	782	15	US-10-190-115-39	Sequence 39, Appl
695	1198.5	29.7	782	15	US-10-369-072-39	Sequence 39, Appl
696	1150.5	28.5	607	14	US-10-320-769-4	Sequence 4, Appli
697	1097	27.2	963	15	US-10-190-115-46	Sequence 46, Appl
698	1097	27.2	963	15	US-10-369-072-46	Sequence 46, Appl
699	1097	27.2	963	15	US-10-042-865-57	Sequence 57, Appl
700	1094	27.1	833	14	US-10-149-819-4	Sequence 4, Appli
701	1090	27.0	833	15	US-10-312-352-31	Sequence 31, Appl

702	1084	26.9	833	15	US-10-190-115-14	Sequence 14, Appl
703	1084	26.9	833	15	US-10-369-072-14	Sequence 14, Appl
704	1083	26.9	833	15	US-10-190-115-16	Sequence 16, Appl
705	1083	26.9	833	15	US-10-190-115-18	Sequence 18, Appl
706	1083	26.9	833	15	US-10-369-072-16	Sequence 16, Appl
707	1083	26.9	833	15	US-10-369-072-18	Sequence 18, Appl
708	1083	26.9	833	15	US-10-403-676-6	Sequence 6, Appli
709	1079.5	26.8	834	10	US-09-759-130B-335	Sequence 335, App
710	1079.5	26.8	834	14	US-10-189-123-65	Sequence 65, Appl
711	1079.5	26.8	834	14	US-10-188-495-65	Sequence 65, Appl
712	1079.5	26.8	834	15	US-10-190-115-47	Sequence 47, Appl
713	1079.5	26.8	834	15	US-10-369-072-47	Sequence 47, Appl
714	1079.5	26.8	834	15	US-10-042-865-58	Sequence 58, Appl
715	1079.5	26.8	834	16	US-10-741-790-335	Sequence 335, App
716	1076	26.7	833	15	US-10-403-676-12	Sequence 12, Appl
717	1067	26.5	634	15	US-10-190-115-120	Sequence 120, App
718	1067	26.5	634	15	US-10-403-676-2	Sequence 2, Appli
719	1067	26.5	638	15	US-10-190-115-123	Sequence 123, App
720	1067	26.5	638	15	US-10-403-676-8	Sequence 8, Appli
721	1066	26.4	638	15	US-10-190-115-125	Sequence 125, App
722	1066	26.4	638	15	US-10-403-676-10	Sequence 10, Appl
723	1062	26.3	861	15	US-10-042-865-61	Sequence 61, Appl
724	1055	26.2	805	15	US-10-042-865-4	Sequence 4, Appli
725	1044	25.9	862	8	US-08-556-422-2	Sequence 2, Appli
726	1044	25.9	862	14	US-10-261-049-2	Sequence 2, Appli
727	1044	25.9	862	14	US-10-320-769-2	Sequence 2, Appli
728	1032.5	25.6	624	13	US-10-003-152-22	Sequence 22, Appl
729	1032.5	25.6	624	14	US-10-002-050-22	Sequence 22, Appl
730	1032.5	25.6	624	14	US-10-002-304-22	Sequence 22, Appl
731	1029.5	25.5	596	13	US-10-003-152-14	Sequence 14, Appl
732	1029.5	25.5	596	14	US-10-002-050-14	Sequence 14, Appl
733	1029.5	25.5	596	14	US-10-002-304-14	Sequence 14, Appl
734	1028.5	25.5	590	13	US-10-003-152-12	Sequence 12, Appl
735	1028.5	25.5	590	14	US-10-002-050-12	Sequence 12, Appl
736	1028.5	25.5	590	14	US-10-002-304-12	Sequence 12, Appl
737	1022.5	25.4	673	9	US-09-908-193-46	Sequence 46, Appl
738	972	24.1	785	9	US-09-989-920-218	Sequence 218, App
739	972	24.1	785	11	US-09-989-890-244	Sequence 244, App
740	961	23.8	865	9	US-09-854-845-33	Sequence 33, Appl
741	958	23.8	838	9	US-09-854-845-29	Sequence 29, Appl
742	958	23.8	838	15	US-10-190-115-49	Sequence 49, Appl
743	958	23.8	838	15	US-10-369-072-49	Sequence 49, Appl
744	954.5	23.7	870	9	US-09-854-845-31	Sequence 31, Appl
745	951.5	23.6	843	9	US-09-854-845-27	Sequence 27, Appl
746	895	22.2	766	9	US-09-854-845-49	Sequence 49, Appl
747	893	22.2	697	9	US-09-854-845-25	Sequence 25, Appl
748	892	22.1	739	9	US-09-854-845-45	Sequence 45, Appl
749	888.5	22.0	771	9	US-09-854-845-47	Sequence 47, Appl
750	886.5	22.0	702	9	US-09-854-845-23	Sequence 23, Appl
751	885.5	22.0	744	9	US-09-854-845-43	Sequence 43, Appl
752	884	21.9	495	15	US-10-403-676-4	Sequence 4, Appli
753	838.5	20.8	753	15	US-10-231-956A-438	Sequence 438, App
754	835.5	20.7	255	15	US-10-312-352-10	Sequence 10, Appl
755	827	20.5	598	9	US-09-854-845-41	Sequence 41, Appl
756	825.5	20.5	771	14	US-10-097-340-284	Sequence 284, App
757	825.5	20.5	771	14	US-10-262-538-10	Sequence 10, Appl
758	825.5	20.5	771	14	US-10-067-632-54	Sequence 54, Appl

759	825.5	20.5	771	14	US-10-247-671-164	Sequence 164, App
760	820.5	20.4	603	9	US-09-854-845-39	Sequence 39, Appl
761	820	20.3	749	14	US-10-262-538-12	Sequence 12, Appl
762	820	20.3	749	14	US-10-285-351B-1	Sequence 1, Appli
763	819.5	20.3	785	14	US-10-262-538-18	Sequence 18, Appl
764	815.5	20.2	655	14	US-10-320-769-3	Sequence 3, Appli
765	810	20.1	737	10	US-09-808-665A-2	Sequence 2, Appli
766	810	20.1	737	10	US-09-808-665A-4	Sequence 4, Appli
1262	793.5	19.7	777	14	US-10-174-587-348	Sequence 348, App
1302	793.5	19.7	777	14	US-10-013-909A-310	Sequence 310, App
1352	793	19.7	431	15	US-10-190-115-97	Sequence 97, Appl
1353	793	19.7	431	15	US-10-369-072-97	Sequence 97, Appl
1354	792.5	19.7	777	15	US-10-404-438-1	Sequence 1, Appli
1355	782.5	19.4	751	13	US-10-114-893-214	Sequence 214, App
1356	782.5	19.4	751	14	US-10-060-036-172	Sequence 172, App
1357	782.5	19.4	751	14	US-10-205-823-359	Sequence 359, App
1358	782.5	19.4	751	14	US-10-262-538-14	Sequence 14, Appl
1359	760.5	18.9	430	11	US-09-964-956-76	Sequence 76, Appl
1360	760.5	18.9	430	15	US-10-190-115-91	Sequence 91, Appl
1361	760.5	18.9	430	15	US-10-369-072-91	Sequence 91, Appl
1362	760.5	18.9	430	15	US-10-087-684-113	Sequence 113, App
1363	760.5	18.9	430	15	US-10-218-779-113	Sequence 113, App
1364	747	18.5	431	15	US-10-087-684-114	Sequence 114, App
1365	747	18.5	431	15	US-10-218-779-114	Sequence 114, App
1366	747	18.5	433	11	US-09-964-956-77	Sequence 77, Appl
1367	738.5	18.3	636	16	US-10-408-765A-2003	Sequence 2003, Ap
1368	737	18.3	782	9	US-09-813-290-4	Sequence 4, Appli
1369	737	18.3	875	9	US-09-813-290-2	Sequence 2, Appli
1370	735.5	18.2	417	15	US-10-042-865-63	Sequence 63, Appl
1371	723.5	17.9	1093	14	US-10-102-524-1858	Sequence 1858, Ap
1372	723.5	17.9	1093	15	US-10-190-115-106	Sequence 106, App
1373	723.5	17.9	1130	15	US-10-190-115-108	Sequence 108, App
1374	723.5	17.9	1151	14	US-10-102-524-1857	Sequence 1857, Ap
1375	723.5	17.9	1202	14	US-10-102-524-1856	Sequence 1856, Ap
1376	723.5	17.9	1202	15	US-10-190-115-45	Sequence 45, Appl
1377	723.5	17.9	1202	15	US-10-369-072-45	Sequence 45, Appl
1378	723.5	17.9	1352	15	US-10-190-115-12	Sequence 12, Appl
1379	723.5	17.9	1352	15	US-10-369-072-12	Sequence 12, Appl
1380	722	17.9	420	15	US-10-042-865-62	Sequence 62, Appl
1381	721.5	17.9	1034	9	US-09-854-845-6	Sequence 6, Appli
1382	721.5	17.9	1049	9	US-09-854-845-2	Sequence 2, Appli
1383	721.5	17.9	1078	9	US-09-854-845-8	Sequence 8, Appli
1392	721.5	17.9	1092	14	US-10-237-535-96	Sequence 96, Appl
1401	721.5	17.9	1092	14	US-10-239-196-96	Sequence 96, Appl
1492	721.5	17.9	1093	9	US-09-854-845-4	Sequence 4, Appli
1493	721.5	17.9	1136	9	US-09-854-845-12	Sequence 12, Appl
1494	721.5	17.9	1151	9	US-09-854-845-10	Sequence 10, Appl
1495	710	17.6	496	9	US-09-854-845-21	Sequence 21, Appl
1496	709.5	17.6	775	13	US-10-144-031-1	Sequence 1, Appli
1497	702.5	17.4	779	9	US-09-731-179-2	Sequence 2, Appli
1498	700.5	17.4	775	14	US-10-262-538-16	Sequence 16, Appl
1499	700.5	17.4	775	14	US-10-177-293-415	Sequence 415, App
1500	700.5	17.4	775	15	US-10-403-676-92	Sequence 92, Appl

Search completed: February 10, 2005, 02:17:39
Job time : 156 secs

OM protein - protein search, using sw model

Run on: February 10, 2005, 02:13:04 ; Search time 179 Seconds
(without alignments)
2177.052 Million cell updates/sec

Title: US-10-015-391A-277
Perfect score: 4031
Sequence: 1 MALPALGLDPWSLLGLFLFQ.....CRTSASDVDADNNCLGTEVA 761

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
1	4031	100.0	761	1	SM4A_HUMAN	Q9h3s1	homo sapien
2	3827	94.9	723	2	Q6MZT6	Q6mzt6	homo sapien
3	3385.5	84.0	760	2	Q66HA9	Q66ha9	rattus norv
4	3280.5	81.4	760	1	SM4A_MOUSE	Q62178	mus musculu
5	1743	43.2	328	2	Q9HA40	Q9ha40	homo sapien
6	1316	32.6	835	2	Q6DCP0	Q6dcp0	xenopus lae
7	1274	31.6	837	2	Q6UXE3	Q6uxe3	homo sapien
8	1271.5	31.5	832	1	SM4B_HUMAN	Q9npr2	homo sapien
9	1246.5	30.9	871	2	Q69ZB7	Q69zb7	mus musculu
10	1239.5	30.7	823	2	Q8BIR6	Q8bir6	mus musculu
11	1198.5	29.7	782	1	SM4B_MOUSE	Q62179	mus musculu
12	1099	27.3	834	2	Q6DCD2	Q6dcd2	xenopus lae
13	1090	27.0	833	1	SM4C_HUMAN	Q9c0c4	homo sapien
14	1079.5	26.8	834	1	SM4C_MOUSE	Q64151	mus musculu
15	1067.5	26.5	550	2	Q8BIC3	Q8bic3	mus musculu

16	1065	26.4	861	2	Q6GTM9	Q6gtm9	mus musculu
17	1062	26.3	861	1	SM4D_MOUSE	O09126	mus musculu
18	1043	25.9	862	1	SM4D_HUMAN	Q92854	homo sapien
19	1034.5	25.7	681	2	Q7Z3N1	Q7z3n1	homo sapien
20	995	24.7	799	2	Q8BJC1	Q8bjc1	mus musculu
21	992.5	24.6	830	2	Q6NRA4	Q6nra4	xenopus lae
22	984	24.4	837	1	SM4G_MOUSE	Q9wuh7	mus musculu
23	958	23.8	838	1	SM4G_HUMAN	Q9ntn9	homo sapien
24	956.5	23.7	755	2	Q69ZB9	Q69zb9	mus musculu
25	919.5	22.8	770	1	SM4F_HUMAN	O95754	homo sapien
26	917	22.7	766	1	SM4E_BRARE	Q9yhx4	brachydanio
27	912	22.6	762	2	Q6DC14	Q6dc14	brachydanio
28	904	22.4	777	1	SM4F_MOUSE	Q9z123	mus musculu
29	901.5	22.4	776	1	SM4F_RAT	Q9z143	rattus norv
30	882	21.9	722	2	Q810B2	Q810b2	mus musculu
31	880.5	21.8	860	1	S3AA_BRARE	Q9w7j1	brachydanio
32	854.5	21.2	756	2	Q8QGU9	Q8qgu9	gallus gall
33	847	21.0	774	2	Q8JIW9	Q8jiw9	xenopus lae
34	841	20.9	785	1	SM3F_MOUSE	O88632	mus musculu
35	840	20.8	772	1	SM3A_RAT	Q63548	rattus norv
36	838	20.8	772	1	SM3A_CHICK	Q90607	gallus gall
37	837.5	20.8	764	1	SM3D_BRARE	Q9w6g6	brachydanio
38	837	20.8	772	1	SM3A_MOUSE	O08665	mus musculu
39	825.5	20.5	771	1	SM3A_HUMAN	Q14563	homo sapien
40	823.5	20.4	785	1	SM3F_HUMAN	Q13275	homo sapien
41	820	20.3	749	1	SM3B_HUMAN	Q13214	homo sapien
42	819	20.3	695	2	Q6DFQ0	Q6dfq0	xenopus tro
43	816.5	20.3	778	1	S3AB_BRARE	Q9w686	brachydanio
44	812	20.1	695	2	Q6PF60	Q6pf60	xenopus lae
45	804.5	20.0	685	2	Q66KH4	Q66kh4	xenopus lae
46	802.5	19.9	751	1	SM3C_MOUSE	Q62181	mus musculu
47	801.5	19.9	751	2	Q6NXW7	Q6nxw7	mus musculu
48	793.5	19.7	777	1	SM3D_HUMAN	O95025	homo sapien
49	793.5	19.7	777	2	Q6UW77	Q6uw77	homo sapien
50	791.5	19.6	751	1	SM3C_CHICK	O42236	gallus gall
51	789.5	19.6	761	1	SM3D_CHICK	Q90663	gallus gall
52	788	19.5	777	2	Q8BMF6	Q8bmf6	mus musculu
53	787	19.5	777	2	Q8BH34	Q8bh34	m mus muscu
54	784.5	19.5	748	1	SM3B_MOUSE	Q62177	mus musculu
55	782.5	19.4	751	1	SM3C_HUMAN	Q99985	homo sapien
56	737	18.3	782	2	Q9NS98	Q9ns98	homo sapien
57	737	18.3	1088	2	Q6PCK8	Q6pck8	xenopus lae
58	723.5	17.9	1093	1	SM5B_HUMAN	Q9p283	homo sapien
59	721.5	17.9	1092	2	Q6UY12	Q6uy12	homo sapien
60	721.5	17.9	1151	2	Q6DD89	Q6dd89	homo sapien
61	709.5	17.6	775	2	Q9QX23	Q9qx23	mus musculu
62	705.5	17.5	725	2	Q7L9D9	Q7l9d9	homo sapien
63	700.5	17.4	775	1	SM3E_HUMAN	O15041	homo sapien
64	700.5	17.4	775	1	SM3E_MOUSE	P70275	mus musculu
65	699	17.3	1122	2	Q7TT33	Q7tt33	mus musculu
66	695.5	17.3	1077	1	SM5A_MOUSE	Q62217	mus musculu
67	694	17.2	1093	1	SM5B_MOUSE	Q60519	mus musculu
68	688.5	17.1	562	2	Q6P1C9	Q6p1c9	mus musculu
69	688.5	17.1	844	2	Q8BXU8	Q8bxu8	m mus muscu
70	679.5	16.9	886	1	SM6B_MOUSE	O54951	mus musculu
71	679.5	16.9	1073	2	Q76KF0	Q76kf0	mus musculu
72	678.5	16.8	587	2	Q8BUT0	Q8but0	mus musculu

73	678.5	16.8	605	2	Q8BXZ7	Q8bxz7	mus musculu
74	678.5	16.8	888	1	SM6A_MOUSE	O35464	mus musculu
75	678.5	16.8	976	2	Q6P5A8	Q6p5a8	mus musculu
76	678.5	16.8	1031	2	Q6PCN9	Q6pcn9	mus musculu
77	677.5	16.8	1074	1	SM5A_HUMAN	Q13591	homo sapien
78	673	16.7	888	1	SM6B_HUMAN	Q9h3t3	homo sapien
79	672.5	16.7	887	1	SM6B_RAT	O70141	rattus norv
80	672.5	16.7	1073	2	Q8NFY4	Q8nfy4	homo sapien
81	671	16.6	1030	1	SM6A_HUMAN	Q9h2e6	homo sapien
82	668	16.6	687	2	Q9BXR8	Q9bxr8	homo sapien
83	662	16.4	785	1	SM3E_CHICK	O42237	gallus gall
84	657.5	16.3	730	1	SM1A_SCHAM	Q26473	schistocerc
85	652.5	16.2	850	1	SM1A_DROME	Q24322	drosophila
86	652	16.2	1017	2	Q8NFY5	Q8nfy5	homo sapien
87	650	16.1	1022	2	Q9P249	Q9p249	homo sapien
88	649.5	16.1	998	2	Q8NFY6	Q8nfy6	homo sapien
89	649.5	16.1	1009	2	Q80TD0	Q80td0	mus musculu
90	647	16.1	1054	2	Q76KF1	Q76kf1	mus musculu
91	645.5	16.0	998	2	Q76KF3	Q76kf3	mus musculu
92	645	16.0	1030	2	Q76KF2	Q76kf2	mus musculu
93	643	16.0	1011	2	Q8NFY3	Q8nfy3	homo sapien
94	642.5	15.9	968	2	Q6P7E1	Q6p7e1	brachydanio
95	642.5	15.9	1005	2	Q9EQ71	Q9eq71	mus musculu
96	641	15.9	1011	2	Q76KF4	Q76kf4	mus musculu
97	635	15.8	595	2	Q8BKG8	Q8bkg8	mus musculu
98	630	15.6	930	1	SM6C_HUMAN	Q9h3t2	homo sapien
99	623.5	15.5	452	2	Q7T165	Q7t165	brachydanio
100	621.5	15.4	712	1	SM1A_CAEEEL	Q17330	caenorhabdi
101	615.5	15.3	963	2	Q91Y36	Q91y36	mus musculu
102	614.5	15.2	931	1	SM6C_MOUSE	Q9wtm3	mus musculu
103	605.5	15.0	697	2	Q6NN47	Q6nn47	drosophila
104	605.5	15.0	960	1	SM6C_RAT	Q9wtl3	rattus norv
105	604	15.0	712	1	SM1A_TRICF	Q26972	tribolium c
106	602.5	14.9	697	2	Q8MLF1	Q8mlf1	drosophila
107	602.5	14.9	724	2	Q9V7Q7	Q9v7q7	drosophila
108	596.5	14.8	695	2	Q7PP64	Q7pp64	anopheles g
109	592	14.7	701	2	Q7KRC9	Q7krc9	drosophila
110	591.5	14.7	706	1	SM2A_DROME	Q24323	drosophila
111	590	14.6	697	1	SM2A_SCHGR	Q9xzc8	schistocerc
112	589	14.6	745	2	Q7Q6P3	Q7q6p3	anopheles g
113	587	14.6	295	1	SM4D_CHICK	Q90665	gallus gall
114	583	14.5	770	2	O44253	O44253	drosophila
115	581	14.4	770	2	Q9V3M4	Q9v3m4	drosophila
116	560	13.9	895	2	Q7PPN1	Q7ppn1	anopheles g
117	556	13.8	418	2	Q96JU9	Q96ju9	homo sapien
118	556	13.8	457	2	Q9HBR1	Q9hbr1	homo sapien
119	554	13.7	403	2	Q8BKQ6	Q8bkq6	mus musculu
120	551	13.7	616	2	Q9V7P8	Q9v7p8	drosophila
121	542	13.4	476	2	Q8NFY7	Q8nfy7	homo sapien
122	525	13.0	600	2	Q7Q552	Q7q552	anopheles g
123	523.5	13.0	923	2	Q8R4U3	Q8r4u3	mus musculu
124	516	12.8	543	2	Q6P5A5	Q6p5a5	homo sapien
125	516	12.8	666	1	SM7A_HUMAN	O75326	homo sapien
126	515.5	12.8	573	2	Q6PI51	Q6pi51	homo sapien
127	515.5	12.8	920	2	Q8R4U4	Q8r4u4	rattus norv
128	507	12.6	676	2	Q6YBW0	Q6ybw0	trichinella
129	503	12.5	664	1	SM7A_MOUSE	Q9qur8	mus musculu

130	496.5	12.3	367	2	Q9HAH9	Q9hah9	homo sapien
131	495	12.3	774	2	Q6ZPG8	Q6zpg8	mus musculu
132	494.5	12.3	1091	2	Q7YU67	Q7yu67	drosophila
133	494.5	12.3	1093	2	Q9VTT0	Q9vtt0	drosophila
134	492.5	12.2	284	2	O54948	O54948	mus musculu
135	486	12.1	510	2	Q9NX92	Q9nx92	homo sapien
136	481.5	11.9	1093	2	Q7QC32	Q7qc32	anopheles g
137	481	11.9	591	2	Q75M97	Q75m97	homo sapien
138	479.5	11.9	574	2	Q6ZQD8	Q6zqd8	mus musculu
139	472.5	11.7	1081	2	Q9U631	Q9u631	drosophila
140	445.5	11.1	296	2	Q9JI29	Q9ji29	rattus norv
141	442.5	11.0	653	2	Q64906	Q64906	alcelaphine
142	439	10.9	366	2	Q7ZV83	Q7zv83	brachydanio
143	419.5	10.4	202	2	Q8UVD5	Q8uvd5	xenopus lae
144	415	10.3	268	2	Q75PK9	Q75pk9	oryzias lat
145	413	10.2	301	2	Q86UJ2	Q86uj2	homo sapien
146	409	10.1	658	2	Q95XP4	Q95xp4	caenorhabdi
147	398	9.9	658	2	Q9NI38	Q9ni38	caenorhabdi
148	382	9.5	583	2	Q6VZT2	Q6vzt2	canarypox v
149	379.5	9.4	612	2	Q70HA3	Q70ha3	fowlpox vir
150	379.5	9.4	612	2	Q9J5F6	Q9j5f6	fowlpox vir
151	348.5	8.6	654	2	Q9TYS4	Q9tys4	caenorhabdi
152	289.5	7.2	240	2	Q69ZE7	Q69ze7	mus musculu
153	285.5	7.1	1871	1	PXA3_HUMAN	P51805	homo sapien
154	281.5	7.0	1905	2	Q91823	Q91823	xenopus lae
155	277	6.9	1872	2	P70208	P70208	mus musculu
156	276	6.8	699	2	Q96SW4	Q96sw4	homo sapien
157	266.5	6.6	1890	2	Q80UG2	Q80ug2	mus musculu
158	263	6.5	1903	2	Q6BEA0	Q6bea0	brachydanio
159	262	6.5	1894	2	P70206	P70206	mus musculu
160	255	6.3	264	2	Q95Q16	Q95q16	caenorhabdi
161	254	6.3	1838	1	PXB2_HUMAN	O15031	homo sapien
162	251	6.2	160	2	Q8AXA8	Q8axa8	gallus gall
163	250.5	6.2	1892	1	PXB3_MOUSE	Q9qy40	mus musculu
164	246.5	6.1	1754	2	Q9UIW2	Q9uiw2	homo sapien
165	242	6.0	1884	2	Q6NVE6	Q6nve6	mus musculu
166	239.5	5.9	1951	2	Q8TA58	Q8ta58	caenorhabdi
167	238.5	5.9	1963	2	O75051	O75051	homo sapien
168	238	5.9	1884	2	P70207	P70207	mus musculu
169	228	5.7	2051	2	O96682	O96682	drosophila
170	228	5.7	2051	2	Q9V4A7	Q9v4a7	drosophila
171	225.5	5.6	1945	2	O96681	O96681	drosophila
172	225.5	5.6	1945	2	Q9V491	Q9v491	drosophila
173	220	5.5	2119	1	PXB1_MOUSE	Q8cjh3	mus musculu
174	218.5	5.4	144	2	Q75M94	Q75m94	homo sapien
175	217	5.4	1909	1	PXB3_HUMAN	Q9ull4	homo sapien
176	212	5.3	2135	1	PXB1_HUMAN	O43157	homo sapien
177	206.5	5.1	1845	2	Q7PSP2	Q7psp2	anopheles g
178	206	5.1	328	2	Q9YHX3	Q9yhx3	brachydanio
179	198.5	4.9	615	2	Q8K2J5	Q8k2j5	mus musculu
180	195.5	4.8	1880	2	Q6DSU3	Q6dsu3	brachydanio
181	191.5	4.8	637	2	Q6NZU7	Q6nzu7	brachydanio
182	191	4.7	1955	2	Q7QEM6	Q7qem6	anopheles g
183	180	4.5	522	2	Q8NEN3	Q8nen3	homo sapien
184	178.5	4.4	287	2	Q75MQ2	Q75mq2	homo sapien
185	176	4.4	333	2	Q8NBN9	Q8nbn9	homo sapien
186	170	4.2	219	2	Q8MYZ9	Q8myz9	drosophila

187	168.5	4.2	1746	2	Q6ZQ83	Q6zq83	mus musculu
188	168.5	4.2	1925	1	PXD1_HUMAN	Q9y4d7	homo sapien
189	168.5	4.2	1925	2	Q68HV1	Q68hvl	mus musculu
190	167.5	4.2	409	2	Q8QMR4	Q8qmr4	cowpox viru
191	166	4.1	1382	2	Q64GK4	Q64gk4	brachydanio
192	164.5	4.1	374	2	Q71RG3	Q71rg3	homo sapien
193	164	4.1	749	2	Q8C3X9	Q8c3x9	mus musculu
194	164	4.1	1205	2	Q8CGW1	Q8cgw1	mus musculu
195	164	4.1	1574	2	Q9QZC2	Q9qzc2	mus musculu
196	160	4.0	492	2	Q6ZW89	Q6zw89	homo sapien
197	159.5	4.0	1764	2	O45657	O45657	caenorhabdi
198	157.5	3.9	399	2	Q8JL80	Q8jl80	ectromelia
199	157.5	3.9	1766	2	Q6BCZ2	Q6bcz2	caenorhabdi
200	153.5	3.8	402	2	Q80DT7	Q80dt7	cowpox viru
201	152.5	3.8	416	2	Q98VP6	Q98vp6	vaccinia vi
202	151.5	3.8	401	2	Q6RZE4	Q6rze4	rabbitpox v
203	151.5	3.8	1568	2	O60486	O60486	homo sapien
204	150.5	3.7	632	2	Q6ZPQ8	Q6zpq8	mus musculu
205	146.5	3.6	403	1	VA39_VACCC	P21062	vaccinia vi
206	145	3.6	441	1	VA39_VACCV	P24764	vaccinia vi
207	145	3.6	552	2	Q6UX61	Q6ux61	homo sapien
208	139.5	3.5	866	2	O24295	O24295	pisum sativ
209	138	3.4	1529	2	Q80TZ7	Q80tz7	mus musculu
210	138	3.4	3190	2	Q93NW7	Q93nw7	streptomyce
211	132.5	3.3	317	2	Q9NTD4	Q9ntd4	homo sapien
212	132.5	3.3	1375	2	Q9W650	Q9w650	xenopus lae
213	132.5	3.3	3192	2	Q9L4W4	Q9l4w4	streptomyce
214	131.5	3.3	507	2	Q96T04	Q96t04	homo sapien
215	131.5	3.3	562	2	Q8NC49	Q8nc49	homo sapien
216	131.5	3.3	562	2	Q96SY4	Q96sy4	homo sapien
217	131.5	3.3	574	2	Q96SM8	Q96sm8	homo sapien
218	129.5	3.2	1369	2	P79950	P79950	xenopus lae
219	128.5	3.2	446	2	Q8Y768	Q8y768	listeria mo
220	128	3.2	1382	2	Q90975	Q90975	gallus gall
221	127.5	3.2	1369	2	P70003	P70003	xenopus lae
222	127	3.2	1425	2	Q9YGM7	Q9ygm7	fugu rubrip
223	126	3.1	61	2	Q8K4M3	Q8k4m3	mus musculu
224	126	3.1	951	2	Q7YU07	Q7yu07	drosophila
225	126	3.1	1505	2	Q8IM99	Q8im99	drosophila
226	122.5	3.0	419	2	Q86M56	Q86m56	drosophila
227	121.5	3.0	429	2	Q6DEW8	Q6dew8	xenopus tro
228	121	3.0	1374	2	Q9YGN0	Q9ygn0	fugu rubrip
229	120	3.0	210	2	Q6J379	Q6j379	vaccinia vi
230	120	3.0	868	2	O24470	O24470	pisum sativ
231	119.5	3.0	446	2	Q71ZN7	Q71zn7	listeria mo
232	119	3.0	1400	1	RON_HUMAN	Q04912	homo sapien
233	119	3.0	4293	2	O08852	O08852	mus musculu
234	118	2.9	867	2	Q6TXF6	Q6txf6	rattus norv
235	118	2.9	1319	2	Q9HCD3	Q9hcd3	homo sapien
236	117	2.9	1328	2	Q9UIW1	Q9uiw1	homo sapien
237	117	2.9	3352	2	Q93H83	Q93h83	streptomyce
238	116.5	2.9	659	2	Q9FV60	Q9fv60	zea mays (m
239	116	2.9	2126	2	P94996	P94996	mycobacteri
240	115.5	2.9	4194	2	Q68BG5	Q68bg5	streptomyce
241	115.5	2.9	4685	2	Q93HJ2	Q93hj2	streptomyce
242	115.5	2.9	5060	2	Q9K5M1	Q9k5m1	anabaena ci
243	115.5	2.9	6145	2	Q93H84	Q93h84	streptomyce

244	115	2.9	295	2	Q80HU1	Q80hu1	vaccinia vi
245	114.5	2.8	1299	2	Q8CHG6	Q8chg6	mus musculu
246	114.5	2.8	2037	2	Q7QFS2	Q7qfs2	anopheles g
247	114	2.8	861	1	LOX3_PEA	P09918	pisum sativ
248	114	2.8	862	2	Q43191	Q43191	solanum tub
249	114	2.8	2126	2	Q7VEV1	Q7vev1	mycobacteri
250	114	2.8	3567	1	ERY2_SACER	Q03132	saccharopol
251	113.5	2.8	1265	2	Q9F847	Q9f847	amycolatops
252	113.5	2.8	1384	2	Q769I5	Q769i5	bos taurus
253	112.5	2.8	862	2	Q43800	Q43800	nicotiana t
254	112.5	2.8	9507	2	Q9EWA1	Q9ewal	streptomyce
255	112	2.8	4283	2	Q9ERV0	Q9erv0	rattus norv
256	111.5	2.8	756	2	O43304	O43304	homo sapien
257	111.5	2.8	1378	1	RON_MOUSE	Q62190	mus musculu
258	111	2.8	525	2	P95618	P95618	rhodocyclus
259	111	2.8	1024	1	PHF8_HUMAN	Q9uppl	homo sapien
260	111	2.8	4928	2	Q9ALM3	Q9alm3	saccharopol
261	111	2.8	7111	2	Q68BG4	Q68bg4	streptomyce
262	110.5	2.7	446	2	Q92BS2	Q92bs2	listeria in
263	110.5	2.7	1025	2	Q7R0I0	Q7r0i0	giardia lam
264	110.5	2.7	7488	2	Q6JHN6	Q6jhn6	saccharopol
265	110	2.7	902	2	Q86MV7	Q86mv7	trypanosoma
266	109.5	2.7	877	2	Q8S6D6	Q8s6d6	oryza sativ
267	109.5	2.7	1204	2	Q8IXB2	Q8ixb2	homo sapien
268	109	2.7	1646	2	Q7WTE3	Q7wte3	streptomyce
269	108.5	2.7	413	2	Q9KUK2	Q9kuk2	vibrio chol
270	108.5	2.7	753	2	Q69MM4	Q69mm4	oryza sativ
271	108.5	2.7	2768	1	THYG_HUMAN	P01266	homo sapien
272	108	2.7	1131	2	Q8PQ81	Q8pq81	xanthomonas
273	108	2.7	5176	2	Q6JHN7	Q6jhn7	saccharopol
274	108	2.7	6797	2	Q9X993	Q9x993	streptomyce
275	107.5	2.7	280	2	Q6UWC6	Q6uwc6	homo sapien
276	107.5	2.7	612	1	PPCK_COREF	Q8fm16	corynebacte
277	107.5	2.7	787	2	Q6I651	Q6i651	oryza sativ
278	107.5	2.7	813	2	Q9I3X9	Q9i3x9	pseudomonas
279	107.5	2.7	1379	1	MET_MOUSE	P16056	mus musculu
280	107	2.7	382	2	Q98MH8	Q98mh8	rhizobium l
281	107	2.7	540	2	Q9M3Z5	Q9m3z5	cicer ariet
282	107	2.7	639	2	Q96P30	Q96p30	homo sapien
283	107	2.7	868	2	Q43817	Q43817	pisum sativ
284	107	2.7	890	2	Q8LMT7	Q8lmt7	oryza sativ
285	106.5	2.6	563	2	Q6Z4A1	Q6z4a1	oryza sativ
286	106.5	2.6	570	2	Q9YCL3	Q9ycl3	aeropyrum p
287	106	2.6	861	2	Q6X5R7	Q6x5r7	nicotiana a
288	106	2.6	861	2	Q6X5R8	Q6x5r8	nicotiana a
289	106	2.6	3519	1	OL56_STRAT	Q07017	streptomyce
290	105.5	2.6	438	2	Q6Y5S0	Q6y5s0	lampetra fl
291	105.5	2.6	553	2	Q75BX1	Q75bx1	ashbya goss
292	105.5	2.6	755	2	Q82V93	Q82v93	nitrosomona
293	105.5	2.6	3816	2	Q9KIV3	Q9kiv3	streptomyce
294	105.5	2.6	6078	2	Q6JHN8	Q6jhn8	saccharopol
295	105	2.6	570	2	O76449	O76449	caenorhabdi
296	104.5	2.6	467	2	Q93IX9	Q93ix9	streptomyce
297	104.5	2.6	669	1	HD10_HUMAN	Q969s8	homo sapien
298	104.5	2.6	845	2	Q6XGN4	Q6xgn4	hepatitis b
299	104	2.6	1001	2	Q75BT1	Q75bt1	ashbya goss
300	104	2.6	1134	2	Q6PCJ2	Q6pcj2	xenopus lae

301	104	2.6	1763	2	Q9TUI6	Q9tui6	monodelphis
302	103.5	2.6	819	1	CADO_HUMAN	Q86up0	homo sapien
303	103.5	2.6	829	2	Q9XID3	Q9xid3	arabidopsis
304	103.5	2.6	1005	1	PHF8_MOUSE	Q80tj7	mus musculu
305	103.5	2.6	1315	2	Q852D0	Q852d0	oryza sativ
306	103.5	2.6	1724	2	Q8CHB6	Q8chb6	mus musculu
307	103.5	2.6	3367	2	Q68BG3	Q68bg3	streptomyce
308	103	2.6	228	2	Q9JF56	Q9jff56	vaccinia vi
309	103	2.6	390	2	Q9W6U5	Q9w6u5	fugu rubrip
310	103	2.6	426	2	Q9REW0	Q9rew0	erwinia chr
311	103	2.6	525	2	Q9JPB5	Q9jpb5	rhodocyclu
312	103	2.6	609	2	Q9LV35	Q9lv35	arabidopsis
313	103	2.6	6266	2	Q6VT93	Q6vt93	symbiont ba
314	102.5	2.5	753	2	Q93ZS6	Q93zs6	arabidopsis
315	102.5	2.5	825	2	Q9YXE4	Q9yxe4	sphaeropsis
316	102.5	2.5	896	2	Q7QZC9	Q7qzc9	giardia lam
317	102.5	2.5	1404	2	Q08757	Q08757	gallus gall
318	102.5	2.5	1558	1	YK83_YEAST	P36028	saccharomyc
319	102.5	2.5	1569	2	O30767	O30767	streptomyce
320	102	2.5	873	2	Q93YI8	Q93yi8	corylus ave
321	102	2.5	1033	2	Q7PVC3	Q7pvc3	anopheles g
322	102	2.5	1375	2	Q9YGM5	Q9ygm5	fugu rubrip
323	102	2.5	1578	2	Q9Y2H3	Q9y2h3	homo sapien
324	102	2.5	5541	2	Q6W5P9	Q6w5p9	streptomyce
325	101.5	2.5	747	1	CTC8_HUMAN	Q9bqn1	homo sapien
326	101.5	2.5	1014	2	Q6ZU69	Q6zu69	homo sapien
327	101	2.5	753	2	Q9C7U8	Q9c7u8	arabidopsis
328	101	2.5	1310	2	Q98WV6	Q98wv6	human herpe
329	101	2.5	1310	2	Q8AZM2	Q8azm2	human herpe
330	101	2.5	1310	2	Q9J3N0	Q9j3n0	human herpe
331	101	2.5	1646	2	Q80TW6	Q80tw6	mus musculu
332	100.5	2.5	876	2	Q41430	Q41430	solanum tub
333	100.5	2.5	950	1	ZCC3_MOUSE	Q8chp0	mus musculu
334	100.5	2.5	1937	2	Q8RJY2	Q8rjy2	stigmatella
335	100	2.5	48	2	Q8K4M4	Q8k4m4	mus musculu
336	100	2.5	496	2	Q96D64	Q96d64	homo sapien
337	100	2.5	951	2	Q90505	Q90505	fundulus he
338	100	2.5	1729	2	Q7VVC2	Q7vvc2	bordetella
339	100	2.5	2386	1	EFL4_HUMAN	Q7z7m0	homo sapien
340	100	2.5	4067	2	Q70AZ7	Q70az7	actinoplane
341	99.5	2.5	657	1	CSP1_CORGL	Q01377	corynebacte
342	99.5	2.5	657	2	Q83ZP3	Q83zp3	corynebacte
343	99.5	2.5	864	1	LOXX_SOYBN	P24095	glycine max
344	99.5	2.5	1207	2	Q8CH86	Q8ch86	mus musculu
345	99.5	2.5	1527	2	Q9VZZ4	Q9vzz4	drosophila
346	99.5	2.5	2406	2	Q7R299	Q7r299	giardia lam
347	99.5	2.5	3554	2	Q7NUA1	Q7nua1	chromobacte
348	99.5	2.5	4150	2	Q9KIV4	Q9kiv4	streptomyce
349	99	2.5	446	2	O60650	O60650	homo sapien
350	99	2.5	484	1	NER4_HUMAN	Q8wvr8	homo sapien
351	99	2.5	642	2	Q9Y7A3	Q9y7a3	coprinus ci
352	99	2.5	653	2	Q9LSB0	Q9lsb0	arabidopsis
353	99	2.5	770	2	Q8WQ41	Q8wq41	leishmania
354	99	2.5	780	2	Q9GYD6	Q9gyd6	leishmania
355	99	2.5	1382	2	Q75ZY9	Q75zy9	canis famil
356	99	2.5	2100	2	O30481	O30481	streptomyce
357	99	2.5	2201	2	Q70KH4	Q70kh4	streptomyce

358	99	2.5	3038	2	Q9Y8A5	Q9y8a5	aspergillus
359	98.5	2.4	553	2	Q65UI2	Q65ui2	mannheimia
360	98.5	2.4	743	2	Q9MAB0	Q9mab0	arabidopsis
361	98.5	2.4	886	2	Q7SEJ4	Q7sej4	neurospora
362	98.5	2.4	1406	2	Q9PVU4	Q9pvu4	cyprinus ca
363	98.5	2.4	3591	2	Q9KIE1	Q9kiel	streptomyce
364	98	2.4	499	2	Q6FI30	Q6fi30	homo sapien
365	98	2.4	597	2	Q9C5S6	Q9c5s6	arabidopsis
366	98	2.4	611	2	Q8W420	Q8w420	arabidopsis
367	98	2.4	618	2	Q6C446	Q6c446	yarrowia li
368	98	2.4	746	2	Q7PYH6	Q7pyh6	anopheles g
369	98	2.4	772	2	Q9AN37	Q9an37	bradyrhizob
370	98	2.4	856	2	Q42780	Q42780	glycine max
371	98	2.4	856	2	Q9M684	Q9m684	phaseolus v
372	98	2.4	876	2	Q42846	Q42846	hordeum vul
373	98	2.4	931	2	Q8NF26	Q8nf26	homo sapien
374	98	2.4	1027	2	Q6YP20	Q6yp20	mus musculu
375	98	2.4	1114	2	Q9BWV1	Q9bwv1	homo sapien
376	98	2.4	1300	2	Q80AC2	Q80ac2	human herpe
377	98	2.4	1302	2	Q80AB9	Q80ab9	human herpe
378	98	2.4	1306	2	Q80AC0	Q80ac0	human herpe
379	98	2.4	1306	2	Q80AC4	Q80ac4	human herpe
380	98	2.4	1310	1	ICP4_VZVD	P09310	varicella-z
381	98	2.4	1310	2	Q98WV4	Q98wv4	human herpe
382	98	2.4	1310	2	Q98WV5	Q98wv5	human herpe
383	98	2.4	1310	2	Q99BW7	Q99bw7	human herpe
384	98	2.4	1310	2	Q6X674	Q6x674	human herpe
385	98	2.4	1310	2	Q775H6	Q775h6	human herpe
386	98	2.4	1310	2	Q8AZM1	Q8azm1	human herpe
387	98	2.4	1310	2	Q9DK02	Q9dk02	human herpe
388	98	2.4	3524	2	Q93H86	Q93h86	streptomyce
389	98	2.4	3564	2	Q82QT5	Q82qt5	streptomyce
390	98	2.4	4067	2	Q6ZZJ4	Q6zzj4	actinoplane
391	97.5	2.4	349	2	Q9N137	Q9n137	ovis aries
392	97.5	2.4	417	2	Q7W0J0	Q7w0j0	bordetella
393	97.5	2.4	544	2	Q8DII7	Q8dii7	synechococc
394	97.5	2.4	613	2	Q8FR00	Q8fr00	corynebacte
395	97.5	2.4	741	1	LOXB_PHAVU	P27481	phaseolus v
396	97.5	2.4	789	2	Q8N2P7	Q8n2p7	homo sapien
397	97.5	2.4	865	1	LOX2_SOYBN	P09439	glycine max
398	97.5	2.4	893	2	Q9Y1Y3	Q9yly3	ephydatia f
399	97.5	2.4	898	2	Q9UFZ4	Q9ufz4	homo sapien
400	97.5	2.4	912	2	Q9DIH2	Q9dih2	human polio
401	97.5	2.4	1115	2	Q6UXJ5	Q6uxj5	homo sapien
402	97.5	2.4	1158	2	Q9UTR5	Q9utr5	schizosacch
403	97.5	2.4	1238	1	PTPJ_MOUSE	Q64455	mus musculu
404	97.5	2.4	1551	2	Q6DT37	Q6dt37	homo sapien
405	97.5	2.4	1664	2	Q9BZE5	Q9bze5	homo sapien
406	97.5	2.4	1686	2	Q6P7J9	Q6p7j9	homo sapien
407	97.5	2.4	2162	2	Q9FB27	Q9fb27	streptomyce
408	97.5	2.4	6048	2	Q93H87	Q93h87	streptomyce
409	97.5	2.4	6396	2	Q9KID7	Q9kid7	streptomyce
410	97.5	2.4	6842	2	Q84G24	Q84g24	streptomyce
411	97.5	2.4	7746	2	Q82QT4	Q82qt4	streptomyce
412	97	2.4	360	2	Q7MV30	Q7mv30	porphyromon
413	97	2.4	439	2	O70188	O70188	rattus norv
414	97	2.4	590	1	THIC_BACSU	P45740	bacillus su

415	97	2.4	599	2	Q41244	Q41244	glycine max
416	97	2.4	610	1	PPCK_CORGL	Q9aem1	corynebacte
417	97	2.4	731	2	Q6L872	Q6l872	prevotella
418	97	2.4	812	2	Q68CH6	Q68ch6	streptomyce
419	97	2.4	1070	2	Q96JG5	Q96jg5	homo sapien
420	97	2.4	1185	2	Q7L8J7	Q7l8j7	homo sapien
421	97	2.4	1621	2	Q13395	Q13395	homo sapien
422	97	2.4	1859	2	Q6V1N9	Q6v1n9	streptomyce
423	97	2.4	2861	2	Q9U1C3	Q9u1c3	leishmania
424	96.5	2.4	508	1	NFIC_HUMAN	P08651	homo sapien
425	96.5	2.4	646	2	Q6MYU0	Q6myu0	aspergillus
426	96.5	2.4	807	2	Q6UW93	Q6uw93	homo sapien
427	96.5	2.4	857	2	Q8GV02	Q8gv02	brassica na
428	96.5	2.4	870	2	Q6UAN0	Q6uan0	tetraodon n
429	96.5	2.4	1310	2	Q99BU9	Q99bu9	human herpe
430	96.5	2.4	1399	2	Q8VDE8	Q8vde8	mus musculu
431	96.5	2.4	1664	2	Q6P3U5	Q6p3u5	homo sapien
432	96.5	2.4	1666	2	Q76N31	Q76n31	homo sapien
433	96.5	2.4	1995	2	Q7QJS8	Q7qjs8	anopheles g
434	96.5	2.4	2207	2	Q70TF4	Q70tf4	human polio
435	96.5	2.4	2215	1	SORL_MOUSE	O88307	m sortilin-
436	96.5	2.4	3435	2	Q84G23	Q84g23	streptomyce
437	96.5	2.4	20925	2	Q8NJX1	Q8njx1	trichoderma
438	96	2.4	127	2	Q8BYL6	Q8byl6	m mus muscu
439	96	2.4	174	2	Q86LT8	Q86lt8	caenorhabdi
440	96	2.4	281	1	DPH5_MOUSE	Q9cwq0	mus musculu
441	96	2.4	281	2	Q6PAC5	Q6pac5	mus musculu
442	96	2.4	605	1	ALS_PAPHA	O02833	papio hamad
443	96	2.4	699	2	Q6D7Q9	Q6d7q9	erwinia car
444	96	2.4	845	2	Q6XGS6	Q6xgs6	hepatitis b
445	96	2.4	874	2	Q9FQF9	Q9fqf9	phaseolus v
446	96	2.4	887	2	Q75V90	Q75v90	aeromonas h
447	96	2.4	887	2	Q659J9	Q659j9	aeromonas p
448	96	2.4	1165	2	Q99XX8	Q99xx8	streptococc
449	96	2.4	1202	2	Q8BNF7	Q8bnf7	mus musculu
450	96	2.4	2260	2	Q76KZ5	Q76kz5	streptomyce
451	96	2.4	3562	2	Q9F829	Q9f829	micromonosp
452	96	2.4	4881	2	Q9S0R3	Q9s0r3	streptomyce
453	95.5	2.4	491	2	Q82H35	Q82h35	streptomyce
454	95.5	2.4	554	2	Q7QMU3	Q7qmu3	anopheles g
455	95.5	2.4	610	2	Q6F5A5	Q6f5a5	corynebacte
456	95.5	2.4	654	2	Q75LH3	Q75lh3	homo sapien
457	95.5	2.4	666	2	Q9SKX3	Q9skx3	arabidopsis
458	95.5	2.4	845	2	Q6XGV4	Q6xgv4	hepatitis b
459	95.5	2.4	873	2	Q8QGM4	Q8qgm4	fundulus he
460	95.5	2.4	881	2	Q93D17	Q93d17	acinetobact
461	95.5	2.4	881	2	Q6FC54	Q6fc54	acinetobact
462	95.5	2.4	1043	1	GRI2_RAT	Q9wtwl	rattus norv
463	95.5	2.4	1060	2	Q6ZTH1	Q6zth1	homo sapien
464	95.5	2.4	1178	2	Q7R1A3	Q7rla3	giardia lam
465	95.5	2.4	1238	2	Q8CIW9	Q8ciw9	mus musculu
466	95.5	2.4	1782	2	Q6ZPG2	Q6zpg2	mus musculu
467	95.5	2.4	1867	2	Q9H8B7	Q9h8b7	homo sapien
468	95.5	2.4	3901	2	Q9N533	Q9n533	caenorhabdi
469	95.5	2.4	4568	1	DYHB_CHLRE	Q39565	chlamydomon
470	95.5	2.4	4829	1	BIR6_HUMAN	Q9nr09	homo sapien
471	95	2.4	391	2	Q7W4G2	Q7w4g2	bordetella

472	95	2.4	870	2	Q7Y1F4	Q7ylf4	oryza sativ
473	95	2.4	878	2	Q6BI96	Q6bi96	debaryomyce
474	95	2.4	979	2	Q6C863	Q6c863	yarrowia li
475	95	2.4	1015	2	Q14521	Q14521	homo sapien
476	95	2.4	1027	2	Q8K1X0	Q8klx0	mus musculu
477	95	2.4	1165	2	Q8NZB0	Q8nzb0	streptococc
478	95	2.4	1310	2	Q9DWX9	Q9dwx9	human herpe
479	95	2.4	1517	2	Q9ES45	Q9es45	rattus norv
480	95	2.4	1526	2	Q6CYY1	Q6cyy1	erwinia car
481	95	2.4	1726	2	Q7WKT6	Q7wkt6	bordetella
482	95	2.4	1729	2	Q7W7E7	Q7w7e7	bordetella
483	95	2.4	1736	2	Q83362	Q83362	murine leuk
484	95	2.4	1924	2	Q7MBL7	Q7mb17	vibrio vuln
485	95	2.4	2314	2	Q94269	Q94269	caenorhabdi
486	95	2.4	3695	1	LMA5_HUMAN	O15230	homo sapien
487	95	2.4	3695	2	Q8TDF8	Q8tdf8	homo sapien
488	94.5	2.3	499	2	Q9XFX1	Q9xfx1	cicer ariet
489	94.5	2.3	517	2	Q6FPS8	Q6fps8	candida gla
490	94.5	2.3	580	2	Q9NWC4	Q9nwc4	homo sapien
491	94.5	2.3	599	2	Q8FEI7	Q8fei7	escherichia
492	94.5	2.3	624	2	Q9ESS6	Q9ess6	rattus norv
493	94.5	2.3	654	2	Q9NW43	Q9nw43	homo sapien
494	94.5	2.3	843	2	Q8H821	Q8h821	oryza sativ
495	94.5	2.3	845	2	Q6XGX5	Q6xgx5	hepatitis b
496	94.5	2.3	849	2	Q9YKR7	Q9ykr7	human immun
497	94.5	2.3	860	2	Q93D13	Q93dl3	acinetobact
498	94.5	2.3	925	1	ERN2_HUMAN	Q76mj5	h serine/th
499	94.5	2.3	1107	2	Q8H1K9	Q8h1k9	arabidopsis
500	94.5	2.3	1114	2	Q96JH8	Q96jh8	homo sapien
501	94.5	2.3	1155	2	Q717V9	Q717v9	triticum ae
502	94.5	2.3	1207	2	Q6NWW9	Q6nww9	mus musculu
503	94.5	2.3	1277	1	CAML_FUGRU	Q98902	fugu rubrip
504	94.5	2.3	1388	2	Q8NET4	Q8net4	homo sapien
505	94.5	2.3	1418	2	Q9P2M8	Q9p2m8	homo sapien
506	94.5	2.3	2214	1	SORL_HUMAN	Q92673	h sortilin-
507	94.5	2.3	2595	2	Q9ALM6	Q9alm6	saccharopol
508	94.5	2.3	4170	2	Q73Z07	Q73z07	mycobacteri
509	94.5	2.3	4177	2	Q9GUP2	Q9gup2	caenorhabdi
510	94.5	2.3	5924	2	Q84BQ4	Q84bq4	pseudomonas
511	94.5	2.3	8817	2	Q53840	Q53840	polyangium
512	94	2.3	391	2	Q7WFY5	Q7wfy5	bordetella
513	94	2.3	396	1	PAR4_MOUSE	O88634	mus musculu
514	94	2.3	615	1	PLK3_RAT	Q9r011	rattus norv
515	94	2.3	645	2	Q7UHL3	Q7uhl3	rhodopirell
516	94	2.3	673	2	Q90YB3	Q90yb3	paralichthy
517	94	2.3	948	2	Q8PL67	Q8pl67	xanthomonas
518	94	2.3	955	1	YNR7_SCHPO	Q9usz2	schizosacch
519	94	2.3	1026	2	Q86T76	Q86t76	homo sapien
520	94	2.3	1221	2	Q7SBQ8	Q7sbq8	neurospora
521	94	2.3	1421	2	Q9KJ00	Q9kj00	polyangium
522	94	2.3	1478	1	BCK1_YEAST	Q01389	saccharomyc
523	94	2.3	2176	2	Q6V4S5	Q6v4s5	mus musculu
524	94	2.3	2629	1	TEP1_MOUSE	P97499	mus musculu
525	94	2.3	2769	1	THYG_BOVIN	P01267	bos taurus
526	94	2.3	3229	2	Q63UE4	Q63ue4	burkholderi
527	94	2.3	4007	1	FRS1_HUMAN	Q86xx4	homo sapien
528	94	2.3	5636	2	Q9N9M2	Q9n9m2	leishmania

529	94	2.3	11096	2	Q9L4W3	Q9l4w3	streptomyce
530	93.5	2.3	285	2	Q9HT67	Q9ht67	pseudomonas
531	93.5	2.3	375	2	Q8DYP2	Q8dyp2	streptococc
532	93.5	2.3	375	2	Q8E499	Q8e499	streptococc
533	93.5	2.3	414	2	Q8TYI7	Q8tyi7	methanopyru
534	93.5	2.3	538	2	Q641Y9	Q641y9	rattus norv
535	93.5	2.3	545	2	Q6NFK5	Q6nfk5	corynebacte
536	93.5	2.3	546	2	Q9Y9L7	Q9y9l7	aeropyrum p
537	93.5	2.3	546	2	Q7PTK2	Q7ptk2	anopheles g
538	93.5	2.3	571	2	Q7SH58	Q7sh58	neurospora
539	93.5	2.3	595	2	Q7N639	Q7n639	photorhabdu
540	93.5	2.3	606	1	ISPG_CHLCV	Q823i7	chlamydophi
541	93.5	2.3	654	2	Q9DBC6	Q9dbc6	mus musculu
542	93.5	2.3	710	2	Q67WV5	Q67wv5	oryza sativ
543	93.5	2.3	770	2	Q6AEZ1	Q6aez1	leifsonia x
544	93.5	2.3	776	2	Q7XTY8	Q7xty8	oryza sativ
545	93.5	2.3	832	2	Q92EI2	Q92ei2	listeria in
546	93.5	2.3	865	1	LOX2_ORYSA	P29250	oryza sativ
547	93.5	2.3	1107	2	Q9LQV2	Q9lqv2	arabidopsis
548	93.5	2.3	1131	2	Q8PDA9	Q8pda9	xanthomonas
549	93.5	2.3	1256	2	Q6BYK1	Q6byk1	debaryomyce
550	93.5	2.3	1310	2	Q993S8	Q993s8	human herpe
551	93.5	2.3	1562	2	Q8SUW6	Q8suw6	encephalito
552	93.5	2.3	1747	2	Q70P93	Q70p93	melittangiu
553	93.5	2.3	1886	2	Q7X504	Q7x504	leptospira
554	93.5	2.3	1938	2	Q7WXH0	Q7wxh0	alcaligenes
555	93.5	2.3	2438	2	Q6V1M8	Q6v1m8	streptomyce
556	93.5	2.3	9234	2	Q7KTP5	Q7ktp5	drosophila
557	93	2.3	339	2	Q983H0	Q983h0	rhizobium l
558	93	2.3	414	2	Q76E49	Q76e49	methylophil
559	93	2.3	439	1	NFIC_MOUSE	P70255	mus musculu
560	93	2.3	509	2	Q9GHE7	Q9ghe7	lophiola au
561	93	2.3	511	2	O06460	O06460	thermus the
562	93	2.3	521	2	Q6CSC5	Q6csc5	kluyveromyc
563	93	2.3	531	2	Q9W6R3	Q9w6r3	fugu rubrip
564	93	2.3	576	1	P80C_HUMAN	P38432	homo sapien
565	93	2.3	622	2	Q811P2	Q811p2	mus musculu
566	93	2.3	694	1	KFC3_HUMAN	Q9bvg8	homo sapien
567	93	2.3	697	2	O24377	O24377	solanum tub
568	93	2.3	718	2	Q8S984	Q8s984	oryza sativ
569	93	2.3	729	2	Q8LQA9	Q8lqa9	oryza sativ
570	93	2.3	733	2	Q8SQ83	Q8sq83	trichosurus
571	93	2.3	764	2	Q6ZNL8	Q6znl8	homo sapien
572	93	2.3	783	2	Q86YJ2	Q86yj2	homo sapien
573	93	2.3	803	2	Q8P500	Q8p500	xanthomonas
574	93	2.3	861	2	O22508	O22508	solanum tub
575	93	2.3	865	2	Q93WZ2	Q93wz2	gossypium h
576	93	2.3	917	2	O81789	O81789	arabidopsis
577	93	2.3	1046	2	Q8G4Q0	Q8g4q0	bifidobacte
578	93	2.3	1067	2	Q9JY67	Q9jy67	neisseria m
579	93	2.3	1159	2	Q8GU71	Q8gu71	oryza sativ
580	93	2.3	1184	2	Q8S028	Q8s028	oryza sativ
581	93	2.3	1329	1	G124_MOUSE	Q91zv8	mus musculu
582	93	2.3	1381	2	Q7UG95	Q7ug95	rhodopirell
583	93	2.3	1592	1	SORL_CHICK	Q98930	g sortilin-
584	93	2.3	1687	2	Q7SC49	Q7sc49	neurospora
585	93	2.3	1711	2	Q8Z019	Q8z019	anabaena sp

586	93	2.3	2035	1	GRIP_MOUSE	Q6gyp7	mus musculu
587	93	2.3	2195	2	Q6MV07	Q6mv07	neurospora
588	93	2.3	2209	2	Q7SH44	Q7sh44	neurospora
589	93	2.3	2343	2	Q7Z516	Q7z516	homo sapien
590	93	2.3	2440	1	NCR1_HUMAN	O75376	homo sapien
591	93	2.3	4077	2	Q939Z0	Q939z0	amycolatops
592	93	2.3	4106	2	Q846X2	Q846x2	streptomyce
593	93	2.3	4391	1	PGBM_HUMAN	P98160	homo sapien
594	93	2.3	4498	2	Q93HE5	Q93he5	streptomyce
595	92.5	2.3	223	2	Q7T5E3	Q7t5e3	cercopithec
596	92.5	2.3	271	2	Q806A9	Q806a9	cercopithec
597	92.5	2.3	328	2	Q86U14	Q86ul4	homo sapien
598	92.5	2.3	435	2	Q64UU4	Q64uu4	bacteroides
599	92.5	2.3	458	2	Q6CAX2	Q6cax2	yarrowia li
600	92.5	2.3	468	2	Q90WM5	Q90wm5	fugu rubrip
601	92.5	2.3	471	2	Q8PSM3	Q8psm3	methanosarc
602	92.5	2.3	485	2	Q6J4H0	Q6j4h0	ginkgo bilo
603	92.5	2.3	508	2	Q7MFJ7	Q7mfj7	vibrio vuln
604	92.5	2.3	511	2	Q8RGB0	Q8rgb0	fusobacteri
605	92.5	2.3	519	2	Q6Q146	Q6q146	bos taurus
606	92.5	2.3	521	2	Q8K2N6	Q8k2n6	mus musculu
607	92.5	2.3	543	2	Q9HOM6	Q9h0m6	homo sapien
608	92.5	2.3	577	2	Q838J9	Q838j9	enterococcu
609	92.5	2.3	643	2	Q87DS2	Q87ds2	xylella fas
610	92.5	2.3	670	2	Q923I7	Q923i7	mus musculu
611	92.5	2.3	700	2	Q7MAF6	Q7maf6	wolinella s
612	92.5	2.3	764	2	Q94JH7	Q94jh7	oryza sativ
613	92.5	2.3	805	2	Q9N2N2	Q9n2n2	caenorhabdi
614	92.5	2.3	809	2	O94527	O94527	schizosacch
615	92.5	2.3	844	2	Q93D12	Q93d12	acinetobact
616	92.5	2.3	865	2	Q9FEQ3	Q9feq3	pisum sativ
617	92.5	2.3	890	2	Q19811	Q19811	caenorhabdi
618	92.5	2.3	961	1	ROB4_RAT	Q80w87	rattus norv
619	92.5	2.3	1186	2	Q8FLG9	Q8flg9	corynebacte
620	92.5	2.3	1270	2	Q7ZYZ0	Q7zyz0	brachydanio
621	92.5	2.3	1333	1	PAD3_MOUSE	Q99nh2	mus musculu
622	92.5	2.3	1470	2	Q9VF24	Q9vf24	drosophila
623	92.5	2.3	1479	2	Q64449	Q64449	mus musculu
624	92.5	2.3	1644	2	Q6NZN1	Q6nzn1	mus musculu
625	92.5	2.3	2150	2	O37086	O37086	peach roset
626	92.5	2.3	2242	2	Q9P2P9	Q9p2p9	homo sapien
627	92.5	2.3	2944	1	CA17_HUMAN	Q02388	homo sapien
628	92.5	2.3	3032	2	Q8J0F7	Q8j0f7	penicillium
629	92.5	2.3	3094	2	Q695L1	Q695l1	homo sapien
630	92.5	2.3	9550	2	Q6W5P6	Q6w5p6	streptomyce
631	92	2.3	132	2	Q8NAS4	Q8nas4	homo sapien
632	92	2.3	317	2	Q6H7C6	Q6h7c6	oryza sativ
633	92	2.3	352	2	Q7N1I7	Q7n1i7	photorhabdu
634	92	2.3	439	2	Q6A9E9	Q6a9e9	propionibac
635	92	2.3	442	2	Q96VI7	Q96vi7	pneumocysti
636	92	2.3	453	2	O75040	O75040	homo sapien
637	92	2.3	490	2	Q9A800	Q9a800	caulobacter
638	92	2.3	495	2	Q7NJP8	Q7njp8	gloeobacter
639	92	2.3	598	1	LIB2_HUMAN	Q8n423	h leukocyte
640	92	2.3	637	1	GIDA_SYNEL	Q8dlf8	synechococc
641	92	2.3	642	2	Q9E204	Q9e204	cercopithec
642	92	2.3	646	2	Q9VY04	Q9vy04	drosophila

643	92	2.3	737	2	Q7UYH2	Q7uyh2	rhodopirell
644	92	2.3	774	2	Q6BDD5	Q6bdd5	coniophora
645	92	2.3	786	1	SN1L_HUMAN	P57059	homo sapien
646	92	2.3	821	2	Q9EPI1	Q9epi1	rattus norv
647	92	2.3	857	1	LOX3_SOYBN	P09186	glycine max
648	92	2.3	997	2	Q92M06	Q92m06	rhizobium m
649	92	2.3	1032	2	Q7NE78	Q7ne78	gloeobacter
650	92	2.3	1043	1	PCL_DROME	Q24459	drosophila
651	92	2.3	1074	2	Q960T8	Q960t8	drosophila
652	92	2.3	1165	2	Q8K5S2	Q8k5s2	streptococc
653	92	2.3	1173	2	Q8J0F4	Q8j0f4	penicillium
654	92	2.3	1210	2	Q6TAS2	Q6tas2	ctenopharyn
655	92	2.3	1273	2	Q9YCA1	Q9ycal	aeropyrum p
656	92	2.3	1307	2	Q8MT77	Q8mt77	drosophila
657	92	2.3	1311	2	Q961K8	Q961k8	drosophila
658	92	2.3	1332	2	Q765X5	Q765x5	paenibacill
659	92	2.3	1342	2	Q9GPP6	Q9gpp6	drosophila
660	92	2.3	1342	2	Q9VPZ7	Q9vpz7	drosophila
661	92	2.3	1514	2	Q9H0B0	Q9h0b0	homo sapien
662	92	2.3	1819	2	Q75A67	Q75a67	ashbya goss
663	92	2.3	1922	2	Q8TTP1	Q8ttp1	methanosarc
664	92	2.3	3686	2	Q93H58	Q93h58	streptomyce
665	92	2.3	4038	2	Q846X3	Q846x3	streptomyce
666	92	2.3	7525	2	Q9KIE0	Q9kie0	streptomyce
667	92	2.3	16990	2	Q6MZA4	Q6mza4	mycobacteri
668	91.5	2.3	223	2	Q805X0	Q805x0	cercopithec
669	91.5	2.3	301	2	Q8R878	Q8r878	thermoanaer
670	91.5	2.3	384	2	Q8CW42	Q8cw42	escherichia
671	91.5	2.3	475	2	Q96LI5	Q96li5	homo sapien
672	91.5	2.3	482	2	Q7QDN9	Q7qdn9	anopheles g
673	91.5	2.3	510	2	Q7XKV4	Q7xkv4	oryza sativ
674	91.5	2.3	528	2	Q9A365	Q9a365	caulobacter
675	91.5	2.3	588	2	Q79JC2	Q79jc2	shewanella
676	91.5	2.3	602	1	TX15_MOUSE	Q70306	mus musculu
677	91.5	2.3	631	1	PLK3_MOUSE	Q60806	mus musculu
678	91.5	2.3	646	2	Q8CBW9	Q8cbw9	mus musculu
679	91.5	2.3	654	2	Q8C4V3	Q8c4v3	mus musculu
680	91.5	2.3	654	2	Q9Z2G1	Q9z2g1	mus musculu
681	91.5	2.3	658	2	Q725W1	Q725w1	desulfovibr
682	91.5	2.3	723	2	Q9P4D5	Q9p4d5	emericeella
683	91.5	2.3	734	2	Q96LA4	Q96la4	homo sapien
684	91.5	2.3	734	2	Q96P31	Q96p31	homo sapien
685	91.5	2.3	740	2	Q96P29	Q96p29	homo sapien
686	91.5	2.3	742	2	Q8N6S2	Q8n6s2	homo sapien
687	91.5	2.3	747	2	Q74FI9	Q74fi9	geobacter s
688	91.5	2.3	760	2	Q8NBU7	Q8nbu7	homo sapien
689	91.5	2.3	772	2	Q852M4	Q852m4	oryza sativ
690	91.5	2.3	804	2	Q69MN9	Q69mn9	oryza sativ
691	91.5	2.3	834	2	Q82DX5	Q82dx5	streptomyce
692	91.5	2.3	858	2	Q851M7	Q851m7	oryza sativ
693	91.5	2.3	859	1	LOX1_ARATH	Q06327	arabidopsis
694	91.5	2.3	862	2	Q9FT17	Q9ft17	lycopersico
695	91.5	2.3	987	2	Q6NRB9	Q6nrb9	xenopus lae
696	91.5	2.3	1001	2	Q6ZQ64	Q6zq64	mus musculu
697	91.5	2.3	1086	1	TDR7_MOUSE	Q8klh1	mus musculu
698	91.5	2.3	1465	2	Q7TP27	Q7tp27	rattus norv
699	91.5	2.3	1732	2	Q7Z443	Q7z443	homo sapien

700	91.5	2.3	1747	2	Q9N8Q1	Q9n8q1	trypanosoma
701	91.5	2.3	2124	2	Q6GVP0	Q6gvp0	mycobacteri
702	91.5	2.3	2164	2	Q70KH5	Q70kh5	streptomyce
703	91.5	2.3	2190	2	Q7R2Z8	Q7r2z8	giardia lam
704	91.5	2.3	2316	1	PTPZ_RAT	Q62656	rattus norv
705	91.5	2.3	5072	2	Q6JD66	Q6jd66	toxoplasma
706	91	2.3	396	2	Q82D46	Q82d46	streptomyce
707	91	2.3	540	1	TBX6_MOUSE	P70327	mus musculu
708	91	2.3	576	2	Q6H4E9	Q6h4e9	oryza sativ
709	91	2.3	621	2	Q6N3K2	Q6n3k2	rhodopseudo
710	91	2.3	627	1	YERO_YEAST	P40053	saccharomyc
711	91	2.3	749	2	Q8KJR6	Q8kjr6	gordonia sp
712	91	2.3	859	2	Q6GQ12	Q6gql2	xenopus lae
713	91	2.3	860	2	Q9M5D3	Q9m5d3	arachis hyp
714	91	2.3	861	1	LOX1_SOLTU	P37831	solanum tub
715	91	2.3	884	2	Q7X9G5	Q7x9g5	fragaria an
716	91	2.3	1010	2	Q9X2G6	Q9x2g6	thermotoga
717	91	2.3	1026	2	Q86T84	Q86t84	homo sapien
718	91	2.3	1027	2	Q90W79	Q90w79	gallus gall
719	91	2.3	1086	2	Q7UIK4	Q7uik4	rhodopirell
720	91	2.3	1093	2	Q8SD16	Q8sd16	pseudomonas
721	91	2.3	1165	2	Q8KLP1	Q8klp1	streptococc
722	91	2.3	1228	1	NARG_BACSU	P42175	bacillus su
723	91	2.3	1332	2	Q6ZPI6	Q6zpi6	mus musculu
724	91	2.3	1620	1	ALK_HUMAN	Q9um73	homo sapien
725	91	2.3	1994	2	Q6ZPP2	Q6zpp2	mus musculu
726	91	2.3	2330	1	EFL4_MOUSE	P60882	mus musculu
727	90.5	2.2	223	2	Q8JYV5	Q8jyv5	cercopithec
728	90.5	2.2	348	1	IRF2_CHICK	Q98925	gallus gall
729	90.5	2.2	349	1	IRF2_HUMAN	P14316	homo sapien
730	90.5	2.2	457	1	CD4_RAT	P05540	rattus norv
731	90.5	2.2	483	2	Q9L6I6	Q9l6i6	streptomyce
732	90.5	2.2	513	2	Q9N4N8	Q9n4n8	caenorhabdi
733	90.5	2.2	522	2	Q83543	Q83543	mokola viru
734	90.5	2.2	527	2	Q73XV8	Q73xv8	mycobacteri
735	90.5	2.2	549	2	Q9Y754	Q9y754	emericella
736	90.5	2.2	659	2	Q871G2	Q871g2	neurospora
737	90.5	2.2	661	2	Q9JKS3	Q9jks3	mus musculu
738	90.5	2.2	710	1	IRA1_MOUSE	Q62406	mus musculu
739	90.5	2.2	711	2	Q8BR10	Q8br10	mus musculu
740	90.5	2.2	732	2	Q8X2C3	Q8x2c3	escherichia
741	90.5	2.2	802	2	Q8IUM7	Q8ium7	homo sapien
742	90.5	2.2	845	2	Q6XGW1	Q6xgw1	hepatitis b
743	90.5	2.2	880	2	Q7R380	Q7r380	giardia lam
744	90.5	2.2	1002	2	Q6CSJ4	Q6csj4	kluveromyc
745	90.5	2.2	1020	2	Q6P1M3	Q6plm3	homo sapien
746	90.5	2.2	1043	2	Q6NXZ1	Q6nxz1	mus musculu
747	90.5	2.2	1076	2	Q6ZM21	Q6zm21	brachydanio
748	90.5	2.2	1078	2	Q80TS9	Q80ts9	mus musculu
749	90.5	2.2	1147	2	Q9DDK1	Q9ddk1	meleagris g
750	90.5	2.2	1156	1	N133_HUMAN	Q8wum0	homo sapien
751	90.5	2.2	1203	2	Q8BXP6	Q8bxp6	mus musculu
752	90.5	2.2	1382	1	MET_RAT	P97523	rattus norv
753	90.5	2.2	1535	2	Q23991	Q23991	drosophila
754	90.5	2.2	2217	2	Q8AV57	Q8av57	gallus gall
755	90.5	2.2	2569	2	O87313	O87313	mycobacteri
756	90	2.2	366	2	Q6LWW5	Q6lww5	methanococc

757	90	2.2	426	1	GUNZ_ERWCH	P07103	erwinia chr
758	90	2.2	454	2	Q8H661	Q8h661	oryza sativ
759	90	2.2	523	2	Q6DCM0	Q6dcm0	xenopus lae
760	90	2.2	607	1	GLMS_AGRT5	Q8ueh1	a glucosami
761	90	2.2	640	2	Q729V5	Q729v5	desulfovibr
762	90	2.2	649	2	Q6C5P8	Q6c5p8	yarrowia li
763	90	2.2	683	1	LCF5_HUMAN	Q9ulc5	homo sapien
764	90	2.2	739	2	Q6UX44	Q6ux44	homo sapien
765	90	2.2	753	2	Q89PD3	Q89pd3	bradyrhizob
766	90	2.2	778	2	Q6CT32	Q6ct32	kluyveromyc
767	90	2.2	802	2	Q8BGD7	Q8bgd7	mus musculu
768	90	2.2	803	2	Q9AUU5	Q9auu5	oryza sativ
769	90	2.2	828	2	Q7S9Q7	Q7s9q7	neurospora
770	90	2.2	839	2	Q43438	Q43438	glycine max
771	90	2.2	853	1	LOX4_SOYBN	P38417	glycine max
772	90	2.2	885	2	Q9VVL2	Q9vvl2	drosophila
773	90	2.2	891	2	Q7T2X3	Q7t2x3	gallus gall
774	90	2.2	893	2	Q8MXK7	Q8mxk7	leishmania
775	90	2.2	913	2	Q95ZD3	Q95zd3	leishmania
776	90	2.2	1004	1	YD83_SCHPO	Q10408	schizosacch
777	90	2.2	1028	2	Q9UQ52	Q9uq52	homo sapien
778	90	2.2	1064	2	Q95U28	Q95u28	drosophila
779	90	2.2	1127	2	Q9TTC1	Q9ttc1	phascolarct
780	90	2.2	1170	2	Q9EWH3	Q9ewh3	streptomyce
781	90	2.2	1262	2	Q7QXK5	Q7qzk5	giardia lam
782	90	2.2	1324	2	Q7TNH6	Q7tnh6	mus musculu
783	90	2.2	1406	2	Q22411	Q22411	caenorhabdi
784	90	2.2	1531	2	O60336	O60336	homo sapien
785	90	2.2	1548	2	Q9VVT7	Q9vvt7	drosophila
786	90	2.2	1579	2	Q695L2	Q695l2	mus musculu
787	90	2.2	1825	2	Q8T9W1	Q8t9w1	dictyosteli
788	90	2.2	2018	2	Q740I1	Q740i1	mycobacteri
789	90	2.2	2262	2	Q9V4P4	Q9v4p4	drosophila
790	90	2.2	2474	2	Q8JUX6	Q8jux6	chikungunya
791	90	2.2	2954	2	Q96898	Q96898	hepatitis g
792	90	2.2	3455	2	Q7WTD6	Q7wtd6	streptomyce
793	90	2.2	3956	2	Q9DLN9	Q9dln9	porcine rep
794	90	2.2	3960	2	Q9DLP0	Q9dlp0	porcine rep
795	90	2.2	6889	2	Q8XS40	Q8xs40	ralstonia s
796	90	2.2	34350	2	Q8WZ42	Q8wz42	homo sapien
797	89.5	2.2	349	1	IRF2_SIGHI	Q8r4e0	sigmodon hi
798	89.5	2.2	409	2	Q61530	Q61530	mus musculu
799	89.5	2.2	422	2	Q7VPV7	Q7vpv7	chlamydia p
800	89.5	2.2	441	2	Q7RY30	Q7ry30	neurospora
801	89.5	2.2	442	1	TOLB_SHEON	Q8edj8	shewanella
802	89.5	2.2	547	2	Q8K2R4	Q8k2r4	mus musculu
803	89.5	2.2	567	2	O05592	O05592	mycobacteri
804	89.5	2.2	567	2	Q7U0V3	Q7u0v3	mycobacteri
805	89.5	2.2	608	2	Q8VKQ0	Q8vkq0	mycobacteri
806	89.5	2.2	615	2	O07437	O07437	mycobacteri
807	89.5	2.2	627	2	Q93IT3	Q93it3	salmonella
808	89.5	2.2	654	2	Q8C0T1	Q8c0t1	mus musculu
809	89.5	2.2	661	2	Q811P4	Q811p4	mus musculu
810	89.5	2.2	699	1	UVRG_HUMAN	Q9p2y5	homo sapien
811	89.5	2.2	699	2	Q6PLX0	Q6plx0	homo sapien
812	89.5	2.2	738	2	Q8AWE4	Q8awe4	petromyzon
813	89.5	2.2	795	2	Q751F8	Q751f8	ashbya goss

814	89.5	2.2	820	2	Q7XZH2	Q7xzh2	oryza sativ
815	89.5	2.2	845	2	Q6XGR2	Q6xgr2	hepatitis b
816	89.5	2.2	866	1	MCM4_DROME	Q26454	drosophila
817	89.5	2.2	866	2	Q39870	Q39870	glycine max
818	89.5	2.2	901	2	Q6IR38	Q6ir38	mus musculu
819	89.5	2.2	975	2	Q9SMB2	Q9smb2	oryza sativ
820	89.5	2.2	1012	1	ROB4_MOUSE	Q8c310	mus musculu
821	89.5	2.2	1041	1	EGT2_YEAST	P42835	saccharomyc
822	89.5	2.2	1288	2	Q75W65	Q75w65	homo sapien
823	89.5	2.2	1330	2	Q7Z494	Q7z494	homo sapien
824	89.5	2.2	1427	2	Q8VIB7	Q8vib7	mesocricetu
825	89.5	2.2	1464	1	NCO2_HUMAN	Q15596	homo sapien
826	89.5	2.2	1472	2	Q95TS6	Q95ts6	drosophila
827	89.5	2.2	1879	2	O30768	O30768	streptomyce
828	89.5	2.2	2163	2	O01912	O01912	caenorhabdi
829	89.5	2.2	2218	2	O09705	O09705	lassa virus
830	89.5	2.2	3649	1	ACVS_NOCLA	P27743	nocardia la
831	89.5	2.2	4207	2	Q7R3Y5	Q7r3y5	giardia lam
832	89	2.2	352	2	Q8PM75	Q8pm75	xanthomonas
833	89	2.2	375	1	GUN_ROBSP	P23044	robillarda
834	89	2.2	437	2	Q6WS86	Q6ws86	streptomyce
835	89	2.2	452	1	FLI1_HUMAN	Q01543	homo sapien
836	89	2.2	469	2	Q7RYR6	Q7ryr6	neurospora
837	89	2.2	487	2	Q9VE73	Q9ve73	drosophila
838	89	2.2	505	2	Q7UME1	Q7umel	rhodopirell
839	89	2.2	520	2	Q875X2	Q875x2	saccharomyc
840	89	2.2	525	1	ATL1_HUMAN	Q8n6g6	homo sapien
841	89	2.2	557	2	Q8S470	Q8s470	zea mays (m
842	89	2.2	568	2	Q8T5H6	Q8t5h6	anopheles g
843	89	2.2	569	2	Q9AXZ3	Q9axz3	persea amer
844	89	2.2	599	2	Q83QD9	Q83qd9	shigella fl
845	89	2.2	677	2	Q6C3K1	Q6c3k1	yarrowia li
846	89	2.2	728	2	Q7R5M3	Q7r5m3	giardia lam
847	89	2.2	759	2	Q8LQG8	Q8lqg8	oryza sativ
848	89	2.2	809	2	Q8UZG7	Q8uzg7	cercopithec
849	89	2.2	825	2	Q8X1Y7	Q8x1y7	metarhizium
850	89	2.2	838	2	Q91C36	Q91c36	hepatitis b
851	89	2.2	843	2	Q76B09	Q76b09	hepatitis b
852	89	2.2	847	1	RSG2_RAT	Q63713	rattus norv
853	89	2.2	848	1	RSG2_MOUSE	P58069	mus musculu
854	89	2.2	860	1	LOXA_LYCES	P38415	lycopersico
855	89	2.2	860	2	Q43190	Q43190	solanum tub
856	89	2.2	861	2	Q9SC16	Q9sc16	solanum tub
857	89	2.2	867	2	Q9JLF9	Q9jlf9	mus musculu
858	89	2.2	875	2	O86394	O86394	neisseria m
859	89	2.2	875	2	Q9K147	Q9k147	neisseria m
860	89	2.2	954	1	SN3B_MOUSE	Q62141	mus musculu
861	89	2.2	1026	2	Q9N6D9	Q9n6d9	leishmania
862	89	2.2	1030	2	Q7SCH0	Q7sch0	neurospora
863	89	2.2	1039	2	Q8X014	Q8x014	neurospora
864	89	2.2	1067	2	Q8BX22	Q8bx22	mus musculu
865	89	2.2	1101	2	Q6A013	Q6a013	mus musculu
866	89	2.2	1130	2	Q9WUC2	Q9wuc2	mus musculu
867	89	2.2	1155	2	Q7QF51	Q7qf51	anopheles g
868	89	2.2	1172	2	Q7TMT3	Q7tmt3	mus musculu
869	89	2.2	1337	1	PAD3_RAT	Q9z340	rattus norv
870	89	2.2	1868	2	Q9VWP3	Q9vwp3	drosophila

871	89	2.2	1953	2	Q9VKD0	Q9vkd0	drosophila
872	89	2.2	2011	2	Q642R6	Q642r6	xenopus lae
873	89	2.2	2768	1	THYG_RAT	P06882	rattus norv
874	89	2.2	3619	2	Q74L43	Q74l43	lactobacill
875	88.5	2.2	217	1	TIM1_RAT	P30120	rattus norv
876	88.5	2.2	249	2	Q7U5Z8	Q7u5z8	synechococc
877	88.5	2.2	337	2	O55825	O55825	sal vieja v
878	88.5	2.2	345	2	Q8IXF6	Q8ixf6	homo sapien
879	88.5	2.2	373	2	Q8X7E1	Q8x7e1	escherichia
880	88.5	2.2	436	2	Q649N9	Q649n9	uncultured
881	88.5	2.2	468	1	MURD_XYLFA	Q9peb0	xylella fas
882	88.5	2.2	495	1	G6PD_STRPN	O54537	streptococc
883	88.5	2.2	495	2	Q8DPK3	Q8dpk3	streptococc
884	88.5	2.2	524	1	TXN2_HUMAN	Q9nnw7	homo sapien
885	88.5	2.2	547	1	RGSE_MOUSE	P97492	mus musculu
886	88.5	2.2	555	2	Q7MDL0	Q7mdl0	vibrio vuln
887	88.5	2.2	598	1	CYSJ_ECOLI	P38038	escherichia
888	88.5	2.2	599	2	Q8X7U1	Q8x7u1	escherichia
889	88.5	2.2	704	2	Q8GZN1	Q8gzn1	arabidopsis
890	88.5	2.2	707	2	Q64CP3	Q64cp3	uncultured
891	88.5	2.2	719	2	Q8TNG2	Q8tng2	methanosarc
892	88.5	2.2	734	2	Q69T58	Q69t58	oryza sativ
893	88.5	2.2	771	2	Q8EP27	Q8ep27	oceanobacil
894	88.5	2.2	802	2	Q8N8S5	Q8n8s5	homo sapien
895	88.5	2.2	815	2	Q8RXU6	Q8rxu6	arabidopsis
896	88.5	2.2	816	2	Q69MM9	Q69mm9	oryza sativ
897	88.5	2.2	839	1	LOX1_SOYBN	P08170	glycine max
898	88.5	2.2	845	2	Q6XGM0	Q6xgm0	hepatitis b
899	88.5	2.2	904	2	Q8A1K1	Q8alk1	bacteroides
900	88.5	2.2	935	1	YHR8_SCHPO	Q8wzk2	schizosacch
901	88.5	2.2	975	2	Q9MLX1	Q9mlx1	arabidopsis
902	88.5	2.2	1011	2	Q9H0F4	Q9h0f4	homo sapien
903	88.5	2.2	1020	2	Q7SZE3	Q7sze3	brachydanio
904	88.5	2.2	1042	2	Q9C0D8	Q9c0d8	homo sapien
905	88.5	2.2	1170	2	Q7WZN9	Q7wzn9	pseudomonas
906	88.5	2.2	1186	2	Q86YC2	Q86yc2	homo sapien
907	88.5	2.2	1238	2	Q8K3Q2	Q8k3q2	mus musculu
908	88.5	2.2	1405	2	Q9CD19	Q9cd19	mycobacteri
909	88.5	2.2	1423	2	Q76I76	Q76i76	homo sapien
910	88.5	2.2	1424	2	Q7QGE8	Q7qge8	anopheles g
911	88.5	2.2	1440	2	O69498	O69498	mycobacteri
912	88.5	2.2	1447	2	Q6FLG8	Q6flg8	candida gla
913	88.5	2.2	1586	2	Q9P2D3	Q9p2d3	homo sapien
914	88.5	2.2	1731	2	Q8TEP8	Q8tep8	homo sapien
915	88.5	2.2	2024	2	Q9EWA3	Q9ewa3	streptomyce
916	88.5	2.2	2030	2	Q747P6	Q747p6	geobacter s
917	88.5	2.2	2220	2	Q6GWS2	Q6gws2	lassa virus
918	88.5	2.2	2238	2	Q846X5	Q846x5	streptomyce
919	88.5	2.2	2326	1	CCAB_DISOM	P56698	discopyge o
920	88.5	2.2	2376	2	Q9FIN7	Q9fin7	arabidopsis
921	88.5	2.2	2425	2	Q95MJ0	Q95mj0	tupaia glis
922	88.5	2.2	2453	1	NCRI_MOUSE	Q60974	mus musculu
923	88.5	2.2	2605	2	Q50858	Q50858	myxococcus
924	88.5	2.2	2811	2	Q7Q434	Q7q434	anopheles g
925	88.5	2.2	3154	2	Q63L14	Q63l14	burkholderi
926	88.5	2.2	4039	2	Q7ZZ46	Q7zz46	brachydanio
927	88.5	2.2	4311	2	Q7YQK5	Q7yqk5	canis famil

928	88.5	2.2	4968	2	Q29621	Q29621	oryctolagus
929	88.5	2.2	4969	1	RYR2_RABIT	P30957	oryctolagus
930	88.5	2.2	7257	2	Q9KIZ7	Q9kiz7	polyangium
931	88.5	2.2	18412	2	Q7ZZ61	Q7zz61	brachydanio
932	88	2.2	142	2	Q8W017	Q8w017	antirrhinum
933	88	2.2	262	2	Q9FT14	Q9ft14	brassica na
934	88	2.2	367	2	Q750R7	Q750r7	ashbya goss
935	88	2.2	380	2	Q6DBU6	Q6dbu6	brachydanio
936	88	2.2	402	2	Q6MHE5	Q6mhe5	bdellovibri
937	88	2.2	413	2	Q8ZKU3	Q8zku3	salmonella
938	88	2.2	415	2	Q6WS95	Q6ws95	streptomyce
939	88	2.2	466	1	G6P2_MYCTU	O06573	mycobacteri
940	88	2.2	467	1	SIL7_HUMAN	Q9y286	homo sapien
941	88	2.2	475	2	Q97EF0	Q97ef0	clostridium
942	88	2.2	583	1	PHBC_AZOCA	O66392	a poly-beta
943	88	2.2	591	1	AGP1_ASCSU	Q17045	ascaris suu
944	88	2.2	617	2	Q7UXH1	Q7uxh1	rhodopirell
945	88	2.2	622	2	Q9JKB2	Q9jkb2	mus musculu
946	88	2.2	631	2	Q9HE62	Q9he62	neurospora
947	88	2.2	650	2	Q942U9	Q942u9	oryza sativ
948	88	2.2	651	2	Q9R687	Q9r687	agrobacteri
949	88	2.2	651	2	Q8U697	Q8u697	agrobacteri
950	88	2.2	652	2	Q8YRC9	Q8yrc9	anabaena sp
951	88	2.2	654	1	BCCA_MYCTU	P46401	mycobacteri
952	88	2.2	674	2	Q6ZKN0	Q6zkn0	oryza sativ
953	88	2.2	695	2	Q9RS56	Q9rs56	deinococcus
954	88	2.2	704	2	Q7POU4	Q7p0u4	chromobacte
955	88	2.2	725	1	MASZ_PSEPK	Q88qx8	pseudomonas
956	88	2.2	789	1	ATX1_RAT	Q63540	rattus norv
957	88	2.2	827	2	Q9H1B6	Q9hlb6	homo sapien
958	88	2.2	835	2	Q902P7	Q902p7	human immun
959	88	2.2	845	2	Q6XGW8	Q6xgw8	hepatitis b
960	88	2.2	854	2	Q7ZAQ0	Q7zaq0	human immun
961	88	2.2	861	2	O24379	O24379	solanum tub
962	88	2.2	873	2	Q65MD5	Q65md5	bacillus li
963	88	2.2	875	2	Q76CF0	Q76cf0	gallus gall
964	88	2.2	912	2	Q6L4G6	Q6l4g6	oryza sativ
965	88	2.2	949	1	IF2_HELPJ	Q9zm46	helicobacte
966	88	2.2	954	2	Q7NC22	Q7nc22	mycoplasma
967	88	2.2	959	2	Q86Y38	Q86y38	homo sapien
968	88	2.2	1041	2	Q7S0H2	Q7s0h2	neurospora
969	88	2.2	1096	2	Q9N9I9	Q9n9i9	leishmania
970	88	2.2	1129	1	AK11_RAT	Q62924	rattus norv
971	88	2.2	1139	1	ARHA_HUMAN	O15013	homo sapien
972	88	2.2	1317	2	Q91Y25	Q91y25	cricetulus
973	88	2.2	1322	2	Q6MKB2	Q6mkb2	bdellovibri
974	88	2.2	1421	2	Q9L8C9	Q9l8c9	polyangium
975	88	2.2	1492	2	Q72IM8	Q72im8	thermus the
976	88	2.2	1548	1	UGGG_DROME	Q09332	drosophila
977	88	2.2	1734	2	Q9J8E2	Q9j8e2	murine leuk
978	88	2.2	1865	2	O81909	O81909	arabidopsis
979	88	2.2	1885	2	Q8RJY4	Q8rjy4	stigmatella
980	88	2.2	1993	2	Q7PS34	Q7ps34	anopheles g
981	88	2.2	2036	1	GRIP_HUMAN	Q6gyq0	homo sapien
982	88	2.2	2332	2	Q6RKE9	Q6rke9	cochliobolu
983	88	2.2	2559	2	O87606	O87606	bacillus su
984	88	2.2	2723	2	O30479	O30479	streptomyce

985	88	2.2	3178	2	Q7UFE9	Q7ufe9	rhodopirell
986	88	2.2	3232	2	O94205	O94205	claviceps p
987	88	2.2	3960	2	Q9DLP1	Q9dlp1	porcine rep
988	88	2.2	4666	2	Q7XQ90	Q7xq90	oryza sativ
989	88	2.2	4861	2	Q15751	Q15751	homo sapien
990	88	2.2	5990	2	Q9RLP6	Q9rlp6	mycobacteri
991	87.5	2.2	304	1	TRUB_PSEAE	P72154	pseudomonas
992	87.5	2.2	304	2	Q6J4L4	Q6j4l4	mycobacteri
993	87.5	2.2	317	2	Q8A5N5	Q8a5n5	bacteroides
994	87.5	2.2	408	2	Q846Q8	Q846q8	myxococcus
995	87.5	2.2	422	2	Q9JSB3	Q9jsb3	chlamydia p
996	87.5	2.2	422	2	Q9Z7H6	Q9z7h6	chlamydia p
997	87.5	2.2	423	2	Q9UBD0	Q9ubd0	homo sapien
998	87.5	2.2	432	2	Q9NPM2	Q9npm2	homo sapien
999	87.5	2.2	451	2	Q8BZ56	Q8bz56	mus musculu
1000	87.5	2.2	533	1	TX15_HUMAN	Q96sf7	homo sapien
1001	87.5	2.2	533	2	Q64S18	Q64s18	bacteroides
1002	87.5	2.2	614	2	Q67SX7	Q67sx7	symbiobacte
1003	87.5	2.2	627	2	Q83SZ5	Q83sz5	salmonella
1004	87.5	2.2	635	2	Q7TST6	Q7tst6	mus musculu
1005	87.5	2.2	676	1	EXL1_HUMAN	Q92935	homo sapien
1006	87.5	2.2	697	2	Q7XJB9	Q7xjb9	oryza sativ
1007	87.5	2.2	722	2	Q9N3N3	Q9n3n3	caenorhabdi
1008	87.5	2.2	743	2	Q8KBW3	Q8kbw3	chlorobium
1009	87.5	2.2	759	2	Q8AAU9	Q8aaau9	bacteroides
1010	87.5	2.2	760	2	Q8JG08	Q8jg08	tetraodon n
1011	87.5	2.2	802	2	Q9SD67	Q9sd67	arabidopsis
1012	87.5	2.2	802	2	Q63TC1	Q63tc1	burkholderi
1013	87.5	2.2	815	2	O64481	O64481	arabidopsis
1014	87.5	2.2	823	2	Q8XEJ0	Q8xej0	escherichia
1015	87.5	2.2	843	1	POL_MLVAK	P03357	akr murine
1016	87.5	2.2	845	2	Q6XGP8	Q6xgp8	hepatitis b
1017	87.5	2.2	852	2	Q8USZ6	Q8usz6	human immun
1018	87.5	2.2	959	2	Q46583	Q46583	desulfovibr
1019	87.5	2.2	1067	2	Q84QV5	Q84qv5	oryza sativ
1020	87.5	2.2	1086	2	Q9N976	Q9n976	leishmania
1021	87.5	2.2	1104	2	Q7MZ50	Q7mz50	photorhabdu
1022	87.5	2.2	1137	2	Q6CAA4	Q6caa4	yarrowia li
1023	87.5	2.2	1288	1	OPLA_MOUSE	Q8k010	mus musculu
1024	87.5	2.2	1613	2	O44368	O44368	drosophila
1025	87.5	2.2	1637	2	Q9W1B0	Q9w1b0	drosophila
1026	87.5	2.2	1709	1	SN_HUMAN	Q9bzz2	homo sapien
1027	87.5	2.2	2113	2	Q7QQZ1	Q7qqz1	giardia lam
1028	87.5	2.2	2134	2	Q8CZT9	Q8czt9	yersinia pe
1029	87.5	2.2	2287	2	Q6RKJ8	Q6rkj8	botrytis ci
1030	87.5	2.2	2503	2	Q99I36	Q99i36	porcine rep
1031	87.5	2.2	2503	2	Q80KX1	Q80kx1	porcine rep
1032	87.5	2.2	2503	2	Q9ENK6	Q9enk6	porcine rep
1033	87.5	2.2	2503	2	Q9WJB2	Q9wjb2	porcine rep
1034	87.5	2.2	3587	1	TYCB_BREPA	O30408	b tyrocidin
1035	87.5	2.2	3960	2	Q9DLN8	Q9dln8	porcine rep
1036	87.5	2.2	4071	2	Q6KDZ1	Q6kdz1	gallus gall
1037	87	2.2	281	2	Q9PKJ1	Q9pkj1	chlamydia m
1038	87	2.2	360	1	HFE_RAT	O35799	rattus norv
1039	87	2.2	427	2	Q9RD11	Q9rd11	streptomyce
1040	87	2.2	428	2	Q66HE2	Q66he2	rattus norv
1041	87	2.2	436	2	Q8ITW6	Q8itw6	caenorhabdi

1042	87	2.2	452	1	FLI1_MOUSE	P26323	mus musculu
1043	87	2.2	454	2	Q70HR6	Q70hr6	podocoryne
1044	87	2.2	459	2	Q8MPK9	Q8mpk9	pacifastacu
1045	87	2.2	470	2	Q8C798	Q8c798	mus musculu
1046	87	2.2	509	2	Q9NW49	Q9nw49	homo sapien
1047	87	2.2	538	1	ENW1_HUMAN	Q9uqf0	h herv-w_7q
1048	87	2.2	546	1	PUT2_AGABI	P78568	agaricus bi
1049	87	2.2	549	2	Q6AH59	Q6ah59	leifsonia x
1050	87	2.2	624	2	Q89YB0	Q89yb0	bradyrhizob
1051	87	2.2	655	2	Q7QFI6	Q7qfi6	anopheles g
1052	87	2.2	683	2	Q9XI23	Q9xi23	arabidopsis
1053	87	2.2	687	2	Q80XS6	Q80xs6	mus musculu
1054	87	2.2	715	1	ZDH5_MOUSE	Q8vdz4	mus musculu
1055	87	2.2	737	2	Q7SG03	Q7sg03	neurospora
1056	87	2.2	772	2	Q7USV7	Q7usv7	rhodopirell
1057	87	2.2	777	2	Q7QVA9	Q7qva9	giardia lam
1058	87	2.2	800	2	Q69ZB5	Q69zb5	mus musculu
1059	87	2.2	818	2	Q72E79	Q72e79	desulfovibr
1060	87	2.2	832	2	Q91S89	Q91s89	hepatitis b
1061	87	2.2	843	2	Q8V0M9	Q8v0m9	hepatitis b
1062	87	2.2	843	2	Q7TDR3	Q7tdr3	hepatitis b
1063	87	2.2	857	2	Q41238	Q41238	solanum tub
1064	87	2.2	864	2	O49150	O49150	solanum tub
1065	87	2.2	917	2	Q8WMT4	Q8wmt4	rousettus a
1066	87	2.2	948	1	HPI1_DEIRA	P56867	deinococcus
1067	87	2.2	987	2	Q8XVM5	Q8xvm5	ralstonia s
1068	87	2.2	999	2	Q8S9T9	Q8s9t9	oryza sativ
1069	87	2.2	1002	2	Q8CJT3	Q8cjt3	streptomyce
1070	87	2.2	1037	1	EPA5_HUMAN	P54756	homo sapien
1071	87	2.2	1081	2	Q8BMA5	Q8bma5	mus musculu
1072	87	2.2	1172	2	Q8CG21	Q8cg21	mus musculu
1073	87	2.2	1190	2	P97573	P97573	rattus norv
1074	87	2.2	1289	1	KJ85_MOUSE	Q80va5	mus musculu
1075	87	2.2	1294	2	Q80TB0	Q80tb0	mus musculu
1076	87	2.2	1353	2	Q8S2I1	Q8s2i1	oryza sativ
1077	87	2.2	1378	2	Q65XR5	Q65xr5	oryza sativ
1078	87	2.2	1639	2	O85019	O85019	mycobacteri
1079	87	2.2	1737	2	Q6T2B9	Q6t2b9	streptomyce
1080	87	2.2	1847	2	Q9X992	Q9x992	streptomyce
1081	87	2.2	2027	2	Q91TW9	Q91tw9	maize rayad
1082	87	2.2	2502	2	Q99AV6	Q99av6	porcine rep
1083	87	2.2	2747	2	Q643C7	Q643c7	streptomyce
1084	87	2.2	2766	1	THYG_MOUSE	O08710	mus musculu
1085	87	2.2	3033	2	Q7T7I7	Q7t7i7	hepatitis c
1086	87	2.2	6146	2	Q93HJ5	Q93hj5	streptomyce
1087	86.5	2.1	223	2	Q805W5	Q805w5	cercopithec
1088	86.5	2.1	248	2	Q64ET7	Q64et7	mesocricetu
1089	86.5	2.1	289	2	Q8P5T9	Q8p5t9	xanthomonas
1090	86.5	2.1	331	2	Q6AY81	Q6ay81	rattus norv
1091	86.5	2.1	349	1	IRF2_MOUSE	P23906	mus musculu
1092	86.5	2.1	349	2	Q923E9	Q923e9	mus musculu
1093	86.5	2.1	350	2	Q67YQ8	Q67yq8	arabidopsis
1094	86.5	2.1	350	2	Q6NPN9	Q6nnp9	arabidopsis
1095	86.5	2.1	365	2	Q656N1	Q656n1	oryza sativ
1096	86.5	2.1	377	2	Q9HIG6	Q9hig6	thermoplasm
1097	86.5	2.1	391	2	Q8YPT8	Q8ypt8	anabaena sp
1098	86.5	2.1	468	1	MURD_XYLFT	Q87ea7	xylella fas

1099	86.5	2.1	484	2	Q87I26	Q87i26	vibrio para
1100	86.5	2.1	492	2	Q8COU8	Q8cOu8	mus musculu
1101	86.5	2.1	493	2	Q7MZF0	Q7mzf0	photorhabdu
1102	86.5	2.1	512	2	Q67UR5	Q67ur5	oryza sativ
1103	86.5	2.1	515	2	Q7UK62	Q7uk62	rhodopirell
1104	86.5	2.1	521	1	CL66_CANFA	O46634	canis famil
1105	86.5	2.1	526	1	TXN2_RAT	Q9z0j5	rattus norv
1106	86.5	2.1	533	2	Q80JS8	Q80js8	blackcurran
1107	86.5	2.1	539	2	Q7UA61	Q7ua61	synechococc
1108	86.5	2.1	547	2	Q9XIA4	Q9xia4	arabidopsis
1109	86.5	2.1	547	2	Q834Z6	Q834z6	enterococcu
1110	86.5	2.1	563	2	Q802X9	Q802x9	brachydanio
1111	86.5	2.1	570	2	Q9AQ21	Q9aq21	bradyrhizob
1112	86.5	2.1	579	2	Q6AGG6	Q6agg6	leifsonia x
1113	86.5	2.1	618	2	Q8BI41	Q8bi41	mus musculu
1114	86.5	2.1	623	2	Q7QND0	Q7qnd0	anopheles g
1115	86.5	2.1	636	2	Q8K3C4	Q8k3c4	mus musculu
1116	86.5	2.1	636	2	Q80XU8	Q80xu8	mus musculu
1117	86.5	2.1	675	1	YMV2_CAEEL	P34504	caenorhabdi
1118	86.5	2.1	675	2	Q8EM43	Q8em43	oceanobacil
1119	86.5	2.1	714	2	Q8COU1	Q8cOu1	mus musculu
1120	86.5	2.1	721	2	Q8BPQ6	Q8bpq6	mus musculu
1121	86.5	2.1	735	2	Q6DE99	Q6de99	xenopus lae
1122	86.5	2.1	741	2	Q8BPQ4	Q8bpq4	mus musculu
1123	86.5	2.1	784	2	Q62AN9	Q62an9	burkholderi
1124	86.5	2.1	810	1	ZCC5_HUMAN	Q9c0b0	homo sapien
1125	86.5	2.1	816	2	Q7QWN8	Q7qwn8	giardia lam
1126	86.5	2.1	823	2	Q7AG19	Q7ag19	escherichia
1127	86.5	2.1	824	2	Q7UYB9	Q7uyb9	rhodopirell
1128	86.5	2.1	828	2	Q8EWP9	Q8ewp9	mycoplasma
1129	86.5	2.1	843	2	Q9QKI5	Q9qki5	human immun
1130	86.5	2.1	948	2	Q6YHB8	Q6yhb8	ambystoma t
1131	86.5	2.1	967	1	ATS1_HUMAN	Q9uhi8	homo sapien
1132	86.5	2.1	967	2	Q8NE26	Q8ne26	homo sapien
1133	86.5	2.1	1054	2	Q7PQV1	Q7pqv1	anopheles g
1134	86.5	2.1	1134	2	Q71B05	Q71b05	brachydanio
1135	86.5	2.1	1160	2	O87710	O87710	clostridium
1136	86.5	2.1	1192	2	Q8BSV0	Q8bsv0	mus musculu
1137	86.5	2.1	1244	2	Q82RP2	Q82rp2	streptomyce
1138	86.5	2.1	1249	2	Q7TMZ9	Q7tmz9	rattus norv
1139	86.5	2.1	1275	2	Q99PW0	Q99pw0	rattus norv
1140	86.5	2.1	1390	1	INSR_AEDAE	Q93105	aedes aegyp
1141	86.5	2.1	1432	2	Q99J86	Q99j86	rattus norv
1142	86.5	2.1	1481	2	Q88CV4	Q88cv4	pseudomonas
1143	86.5	2.1	1562	2	O60034	O60034	botrytis ci
1144	86.5	2.1	1575	2	P94904	P94904	lysobacter.
1145	86.5	2.1	2146	2	O59897	O59897	aspergillus
1146	86.5	2.1	2146	2	O60026	O60026	aspergillus
1147	86.5	2.1	2258	2	Q9K5M2	Q9k5m2	anabaena ci
1148	86.5	2.1	3577	2	Q7YV66	Q7yv66	trypanosoma
1149	86.5	2.1	3718	1	LMA5_MOUSE	Q61001	mus musculu
1150	86.5	2.1	4735	2	O54666	O54666	amycolatops
1151	86	2.1	243	2	Q8ITW5	Q8itw5	caenorhabdi
1152	86	2.1	290	2	Q6ZK11	Q6zk11	oryza sativ
1153	86	2.1	291	2	Q6EE24	Q6ee24	siniperca c
1154	86	2.1	296	2	Q842M9	Q842m9	vibrio chol
1155	86	2.1	326	2	Q98V82	Q98v82	hepatitis c

1156	86	2.1	335	2	Q9LX44	Q9lx44	arabidopsis
1157	86	2.1	339	2	Q9FF67	Q9ff67	arabidopsis
1158	86	2.1	363	2	Q9BJ44	Q9bj44	leishmania
1159	86	2.1	399	1	HPPD_COCIM	Q00415	coccidioide
1160	86	2.1	443	2	Q9ZHL4	Q9zhl4	haemophilus
1161	86	2.1	464	2	Q8BLX8	Q8blx8	mus musculu
1162	86	2.1	489	2	Q8BLY0	Q8bly0	m mus muscu
1163	86	2.1	490	2	Q70NV9	Q70nv9	suberites d
1164	86	2.1	500	2	Q6MH10	Q6mh10	bdellovibri
1165	86	2.1	508	2	Q43149	Q43149	sambucus ni
1166	86	2.1	522	2	Q6INM1	Q6inm1	xenopus lae
1167	86	2.1	540	2	Q915C8	Q915c8	human calic
1168	86	2.1	541	2	Q9NTD7	Q9ntd7	homo sapien
1169	86	2.1	550	2	O70621	O70621	mus musculu
1170	86	2.1	553	2	Q7VLE7	Q7vle7	haemophilus
1171	86	2.1	568	2	Q8MU75	Q8mu75	anopheles g
1172	86	2.1	609	2	Q9NVN4	Q9nvn4	homo sapien
1173	86	2.1	611	2	Q7SDI5	Q7sdi5	neurospora
1174	86	2.1	616	2	Q7PXU7	Q7pxu7	anopheles g
1175	86	2.1	620	2	Q98329	Q98329	molluscum c
1176	86	2.1	622	2	Q9ESS5	Q9ess5	mus musculu
1177	86	2.1	623	2	Q6CID5	Q6cid5	kluveromyc
1178	86	2.1	627	2	Q8ZRL9	Q8zrl9	salmonella
1179	86	2.1	723	2	Q8Y6F8	Q8y6f8	listeria mo
1180	86	2.1	723	2	Q9I2M1	Q9i2m1	pseudomonas
1181	86	2.1	724	2	Q74D95	Q74d95	geobacter s
1182	86	2.1	745	2	Q6GMS4	Q6gms4	homo sapien
1183	86	2.1	746	1	EXT1_HUMAN	Q16394	h exostosin
1184	86	2.1	756	2	Q8BNP0	Q8bnp0	mus musculu
1185	86	2.1	756	2	Q9JHE3	Q9jhe3	mus musculu
1186	86	2.1	775	1	RIR1_VZVD	P09248	varicella-z
1187	86	2.1	775	2	Q7QWZ4	Q7qwz4	giardia lam
1188	86	2.1	775	2	Q6QCN6	Q6qcn6	human herpe
1189	86	2.1	775	2	Q6QCV8	Q6qcv8	human herpe
1190	86	2.1	786	2	Q7NN47	Q7nn47	gloeobacter
1191	86	2.1	790	2	Q9HAH2	Q9hah2	homo sapien
1192	86	2.1	791	2	Q6PFJ7	Q6pfj7	brachydanio
1193	86	2.1	795	2	Q8BZ61	Q8bz61	mus musculu
1194	86	2.1	802	2	Q8CJH6	Q8cjh6	rattus norv
1195	86	2.1	816	2	Q9SZV5	Q9szv5	arabidopsis
1196	86	2.1	837	2	Q7THQ4	Q7thq4	hepatitis b
1197	86	2.1	842	2	Q7QFJ1	Q7qfj1	anopheles g
1198	86	2.1	844	2	Q9SAP1	Q9sap1	solanum tub
1199	86	2.1	845	2	Q9WRK8	Q9wrk8	hepatitis b
1200	86	2.1	861	2	Q43189	Q43189	solanum tub
1201	86	2.1	881	2	Q6RSN2	Q6rsn2	carica papa
1202	86	2.1	890	2	Q9Z1A0	Q9z1a0	cavia porce
1203	86	2.1	915	2	Q716L6	Q716l6	mycobacteri
1204	86	2.1	960	2	Q8XWL6	Q8xwl6	ralstonia s
1205	86	2.1	974	2	Q6ABZ1	Q6abz1	leifsonia x
1206	86	2.1	1004	2	O84646	O84646	chlamydia t
1207	86	2.1	1011	2	Q9L5M2	Q9l5m2	salmonella
1208	86	2.1	1011	2	Q935H0	Q935h0	salmonella
1209	86	2.1	1058	1	PMA1_DICDI	P54679	dictyosteli
1210	86	2.1	1067	2	Q9JT51	Q9jt51	neisseria m
1211	86	2.1	1087	2	Q8NEK7	Q8nek7	homo sapien
1212	86	2.1	1161	2	Q9JVR9	Q9jvr9	neisseria m

1213	86	2.1	1206	2	Q6P3S9	Q6p3s9	homo sapien
1214	86	2.1	1214	2	Q9P2G1	Q9p2g1	homo sapien
1215	86	2.1	1253	2	O97566	O97566	canis famil
1216	86	2.1	1332	2	Q7G9P4	Q7g9p4	arabidopsis
1217	86	2.1	1354	2	Q8L4G7	Q8l4g7	oryza sativ
1218	86	2.1	1393	2	Q7XQF9	Q7xqf9	oryza sativ
1219	86	2.1	1420	2	Q6AX68	Q6ax68	xenopus lae
1220	86	2.1	1439	1	PTPK_HUMAN	Q15262	homo sapien
1221	86	2.1	1778	2	Q9NE65	Q9ne65	leishmania
1222	86	2.1	1811	2	O36184	O36184	plautia sta
1223	86	2.1	1827	2	P96203	P96203	mycobacteri
1224	86	2.1	1827	2	Q7TXL7	Q7txl7	mycobacteri
1225	86	2.1	2060	2	Q7YUN5	Q7yun5	trypanosoma
1226	86	2.1	2060	2	Q7YUN7	Q7yun7	trypanosoma
1227	86	2.1	2069	2	Q8NSD9	Q8nsd9	corynebacte
1228	86	2.1	2100	2	Q6M743	Q6m743	corynebacte
1229	86	2.1	2714	2	Q7X325	Q7x325	uncultured
1230	86	2.1	2898	2	Q9VLT6	Q9vlt6	drosophila
1231	86	2.1	5899	2	Q74GG7	Q74gg7	geobacter s
1232	86	2.1	7962	2	Q10465	Q10465	homo sapien
1233	86	2.1	14130	2	Q6MZ72	Q6mz72	mycobacteri
1234	85.5	2.1	139	2	Q6ZWH3	Q6zwh3	homo sapien
1235	85.5	2.1	194	2	Q9RWZ2	Q9rwz2	deinococcus
1236	85.5	2.1	258	2	Q8MII2	Q8mii2	bos taurus
1237	85.5	2.1	282	2	Q7PFX3	Q7pfx3	anopheles g
1238	85.5	2.1	407	2	Q9LR58	Q9lr58	arabidopsis
1239	85.5	2.1	416	2	Q93YX1	Q93yx1	arabidopsis
1240	85.5	2.1	418	1	NER3_MOUSE	Q9jmh7	mus musculu
1241	85.5	2.1	422	2	Q6VMH8	Q6vmh8	streptomyce
1242	85.5	2.1	479	1	GATB_DEIRA	Q9rrd7	deinococcus
1243	85.5	2.1	489	2	Q96BZ4	Q96bz4	homo sapien
1244	85.5	2.1	506	1	NFIC_PIG	P21999	sus scrofa
1245	85.5	2.1	509	2	Q43795	Q43795	nicotiana t
1246	85.5	2.1	520	2	Q925P2	Q925p2	mus musculu
1247	85.5	2.1	527	2	Q65E49	Q65e49	bacillus li
1248	85.5	2.1	538	2	Q8DJE5	Q8dje5	synechococc
1249	85.5	2.1	583	1	CL66_BOVIN	Q9bh13	bos taurus
1250	85.5	2.1	595	1	ARH8_MOUSE	Q9z206	mus musculu
1251	85.5	2.1	597	1	SILL_PANTR	Q95lh0	pan troglod
1252	85.5	2.1	620	2	Q8JFF8	Q8jff8	brachydanio
1253	85.5	2.1	627	2	Q75PK5	Q75pk5	lotus japon
1254	85.5	2.1	650	2	Q6BLJ2	Q6blj2	debaryomyce
1255	85.5	2.1	674	2	Q6C8L7	Q6c8l7	yarrowia li
1256	85.5	2.1	685	1	TRFE_PAROL	O93429	paralichthy
1257	85.5	2.1	696	2	Q8T021	Q8t021	drosophila
1258	85.5	2.1	696	2	Q9VUZ6	Q9vuz6	drosophila
1259	85.5	2.1	738	2	Q6DFA9	Q6dfa9	xenopus lae
1260	85.5	2.1	753	2	Q9SZM2	Q9szm2	arabidopsis
1261	85.5	2.1	823	2	Q7DBG4	Q7dbg4	escherichia
1262	85.5	2.1	832	2	Q7T668	Q7t668	hepatitis b
1263	85.5	2.1	849	2	Q9YKS2	Q9yks2	human immun
1264	85.5	2.1	862	2	Q6GP97	Q6gp97	xenopus lae
1265	85.5	2.1	881	2	Q93VJ2	Q93vj2	arabidopsis
1266	85.5	2.1	881	2	Q94IG5	Q94ig5	arabidopsis
1267	85.5	2.1	894	2	Q8EGB1	Q8egb1	shewanella
1268	85.5	2.1	916	2	Q6ZC33	Q6zc33	oryza sativ
1269	85.5	2.1	939	2	Q9FIN6	Q9fin6	arabidopsis

1270	85.5	2.1	956	2	Q9PJF0	Q9pjf0	chlamydia m
1271	85.5	2.1	974	2	Q8SQP5	Q8sqp5	encephalito
1272	85.5	2.1	1072	2	O94537	O94537	schizosacch
1273	85.5	2.1	1072	2	Q63XR8	Q63xr8	burkholderi
1274	85.5	2.1	1140	2	Q7S718	Q7s718	neurospora
1275	85.5	2.1	1205	2	Q7YSG7	Q7ysg7	sus scrofa
1276	85.5	2.1	1206	2	Q6PW36	Q6pw36	rattus norv
1277	85.5	2.1	1243	2	Q80XH2	Q80xh2	mus musculu
1278	85.5	2.1	1258	2	Q6MLC4	Q6mlc4	bdellovibri
1279	85.5	2.1	1270	2	Q9VBJ3	Q9vbj3	drosophila
1280	85.5	2.1	1333	2	Q8A167	Q8a167	bacteroides
1281	85.5	2.1	1362	2	Q7S0Q7	Q7s0q7	neurospora
1282	85.5	2.1	1440	2	Q68DT8	Q68dt8	homo sapien
1283	85.5	2.1	1670	2	Q7QX76	Q7qx76	giardia lam
1284	85.5	2.1	1706	2	Q6FJN7	Q6fjn7	candida gla
1285	85.5	2.1	1758	2	Q8CHN9	Q8chn9	rattus norv
1286	85.5	2.1	1820	2	Q6C6Q4	Q6c6q4	yarrowia li
1287	85.5	2.1	2061	2	Q9VUH9	Q9vuh9	drosophila
1288	85.5	2.1	2103	2	Q7KUL0	Q7kul0	drosophila
1289	85.5	2.1	2205	1	POLG_POL2W	P23069	p genome po
1290	85.5	2.1	2346	2	Q7RWC7	Q7rwc7	neurospora
1291	85.5	2.1	2541	2	Q8AWI0	Q8awi0	gallus gall
1292	85.5	2.1	3014	2	Q86614	Q86614	hepatitis c
1293	85.5	2.1	3313	1	CLR3_RAT	O88278	rattus norv
1294	85.5	2.1	3534	2	O39266	O39266	equid herpe
1295	85.5	2.1	3939	2	Q93HJ3	Q93hj3	streptomyce
1296	85.5	2.1	4317	2	Q88F56	Q88f56	pseudomonas
1297	85.5	2.1	4869	2	Q90985	Q90985	gallus gall
1298	85.5	2.1	4967	1	RYR2_HUMAN	Q92736	homo sapien
1299	85.5	2.1	4967	2	Q9ERN6	Q9ern6	mus musculu
1300	85.5	2.1	9510	2	Q93NX9	Q93nx9	streptomyce
1301	85.5	2.1	23015	2	Q8IQ18	Q8iq18	drosophila
1302	85	2.1	225	2	Q805W0	Q805w0	cercopithec
1303	85	2.1	234	2	Q6VR10	Q6vr10	theobroma c
1304	85	2.1	268	2	Q8SP82	Q8sp82	gorilla gor
1305	85	2.1	304	2	Q68WL1	Q68wl1	rickettsia
1306	85	2.1	372	1	LIG8_PHACH	P06181	phanerochae
1307	85	2.1	396	2	Q8BZ77	Q8bz77	mus musculu
1308	85	2.1	423	2	Q8ND46	Q8nd46	homo sapien
1309	85	2.1	426	1	PSG8_HUMAN	Q9uq74	homo sapien
1310	85	2.1	432	2	Q7U8Y8	Q7u8y8	synechococc
1311	85	2.1	438	1	GAT3_BRARE	Q91428	brachydanio
1312	85	2.1	441	2	Q86UN2	Q86un2	homo sapien
1313	85	2.1	441	2	Q7R4E2	Q7r4e2	giardia lam
1314	85	2.1	446	2	Q86QI4	Q86qi4	ancylostoma
1315	85	2.1	454	2	Q8Y7C7	Q8y7c7	listeria mo
1316	85	2.1	458	2	Q9VB06	Q9vb06	drosophila
1317	85	2.1	472	2	Q6PIZ7	Q6piz7	homo sapien
1318	85	2.1	499	2	Q72WJ2	Q72wj2	desulfovibr
1319	85	2.1	499	2	Q8FC60	Q8fc60	escherichia
1320	85	2.1	505	2	Q7UGI8	Q7ugi8	rhodopirell
1321	85	2.1	512	2	Q81DX3	Q81dx3	bacillus ce
1322	85	2.1	519	2	Q7ZYH5	Q7zyh5	xenopus lae
1323	85	2.1	555	2	Q6ZMF0	Q6zmf0	homo sapien
1324	85	2.1	555	2	Q9W0K2	Q9w0k2	drosophila
1325	85	2.1	557	2	Q9T6Z6	Q9t6z6	schisandra
1326	85	2.1	569	2	Q7UB02	Q7ub02	shigella fl

1327	85	2.1	572	2	Q68LQ7	Q68lq7	populus max
1328	85	2.1	577	2	Q83J13	Q83j13	shigella fl
1329	85	2.1	579	2	Q68LU0	Q68lu0	humiria bal
1330	85	2.1	596	2	Q93896	Q93896	caenorhabdi
1331	85	2.1	600	2	Q811F5	Q811f5	mus musculu
1332	85	2.1	607	2	Q9T6Z7	Q9t6z7	kadsura jap
1333	85	2.1	607	2	Q726F2	Q726f2	desulfovibr
1334	85	2.1	621	2	Q9EYI3	Q9eyi3	streptomyce
1335	85	2.1	622	2	Q9R069	Q9r069	mus musculu
1336	85	2.1	631	2	O86724	O86724	streptomyce
1337	85	2.1	633	2	Q9Y3W8	Q9y3w8	homo sapien
1338	85	2.1	637	2	Q9HLM9	Q9hlm9	thermoplasm
1339	85	2.1	641	2	Q88E58	Q88e58	pseudomonas
1340	85	2.1	650	2	Q99K86	Q99k86	mus musculu
1341	85	2.1	652	2	Q7R112	Q7r112	giardia lam
1342	85	2.1	653	1	DEND_RAT	P50617	rattus norv
1343	85	2.1	685	2	Q7NIR6	Q7nir6	gloeobacter
1344	85	2.1	690	2	Q9Y2P5	Q9y2p5	homo sapien
1345	85	2.1	698	2	Q8WV40	Q8wv40	homo sapien
1346	85	2.1	699	1	E75_MANSE	Q08893	manduca sex
1347	85	2.1	713	2	Q9YH34	Q9yh34	xenopus lae
1348	85	2.1	715	1	ZDH5_HUMAN	Q9c0b5	homo sapien
1349	85	2.1	727	2	Q9ULL7	Q9ull7	homo sapien
1350	85	2.1	735	2	P90827	P90827	caenorhabdi
1351	85	2.1	749	2	O23045	O23045	arabidopsis
1352	85	2.1	809	2	Q96D36	Q96d36	homo sapien
1353	85	2.1	820	2	Q8AAE0	Q8aae0	bacteroides
1354	85	2.1	841	2	Q9NEA5	Q9nea5	leishmania
1355	85	2.1	843	2	Q918I7	Q918i7	hepatitis b
1356	85	2.1	843	2	Q99HT7	Q99ht7	hepatitis b
1357	85	2.1	853	2	Q43446	Q43446	glycine max
1358	85	2.1	858	2	O04919	O04919	vicia faba
1359	85	2.1	860	2	Q95LZ6	Q95lz6	macaca fasc
1360	85	2.1	865	2	Q6E7H3	Q6e7h3	human immun
1361	85	2.1	900	2	Q6NT70	Q6nt70	homo sapien
1362	85	2.1	908	2	Q8BMI4	Q8bmi4	m mus muscu
1363	85	2.1	908	2	Q8C0J0	Q8c0j0	m mus muscu
1364	85	2.1	964	2	Q6P4G0	Q6p4g0	homo sapien
1365	85	2.1	991	1	RCQ5_HUMAN	O94762	homo sapien
1366	85	2.1	1001	2	Q8VDG6	Q8vdg6	mus musculu
1367	85	2.1	1020	2	Q28390	Q28390	equus cabal
1368	85	2.1	1029	2	Q6UX74	Q6ux74	homo sapien
1369	85	2.1	1039	1	M2C1_MOUSE	Q91w89	mus musculu
1370	85	2.1	1039	2	Q8BWY6	Q8bwy6	mus musculu
1371	85	2.1	1043	2	O17644	O17644	caenorhabdi
1372	85	2.1	1057	2	Q15334	Q15334	homo sapien
1373	85	2.1	1172	1	TSP2_MOUSE	Q03350	mus musculu
1374	85	2.1	1267	1	Z592_HUMAN	Q92610	homo sapien
1375	85	2.1	1313	2	Q80WC1	Q80wc1	mus musculu
1376	85	2.1	1328	2	Q6UAU7	Q6uau7	bacterioph
1377	85	2.1	1332	2	Q7GD73	Q7gd73	arabidopsis
1378	85	2.1	1338	2	Q8PA64	Q8pa64	xanthomonas
1379	85	2.1	1349	2	O23888	O23888	zea mays (m
1380	85	2.1	1352	2	Q70CQ4	Q70cq4	homo sapien
1381	85	2.1	1377	2	Q9P2A8	Q9p2a8	homo sapien
1382	85	2.1	1455	1	GTFC_STRMU	P13470	streptococc
1383	85	2.1	1650	2	Q75C55	Q75c55	ashbya goss

1384	85	2.1	1662	2	Q98TS6	Q98ts6	anarhichas
1385	85	2.1	1777	2	O89278	O89278	himetobi p
1386	85	2.1	1832	2	Q90X04	Q90x04	larus argen
1387	85	2.1	1876	2	Q9R686	Q9r686	bacillus su
1388	85	2.1	1933	2	Q6V3A4	Q6v3a4	mus musculu
1389	85	2.1	1935	1	ATS9_HUMAN	Q9p2n4	homo sapien
1390	85	2.1	2159	2	Q6PAL2	Q6pal2	mus musculu
1391	85	2.1	2210	2	Q6RSS2	Q6rss2	pirital vir
1392	85	2.1	2213	1	SORL_RABIT	Q95209	o sortilin-
1393	85	2.1	2218	2	Q8RJY1	Q8rjy1	stigmatella
1394	85	2.1	2273	2	Q63HU2	Q63hu2	burkholderi
1395	85	2.1	2395	2	Q27167	Q27167	paramecium
1396	85	2.1	2576	2	Q6MN16	Q6mn16	bdellovibri
1397	85	2.1	3010	2	Q68533	Q68533	hepatitis c
1398	85	2.1	3059	2	Q9QBT5	Q9qbt5	potato viru
1399	85	2.1	3179	2	Q6TEI0	Q6tei0	streptomyce
1400	85	2.1	3295	2	Q83X71	Q83x71	streptomyce
1401	85	2.1	10820	2	Q7SDK2	Q7sdk2	neurospora
1402	84.5	2.1	278	2	O53555	O53555	mycobacteri
1403	84.5	2.1	278	2	Q7TWC1	Q7twc1	mycobacteri
1404	84.5	2.1	318	2	Q82XX5	Q82xx5	nitrosomona
1405	84.5	2.1	350	2	Q8TVT5	Q8tvt5	methanopyru
1406	84.5	2.1	385	2	Q9I2P1	Q9i2p1	pseudomonas
1407	84.5	2.1	388	2	Q97BI4	Q97bi4	thermoplasm
1408	84.5	2.1	391	2	Q6EV66	Q6ev66	bos taurus
1409	84.5	2.1	399	2	Q8GVC7	Q8gvc7	phytophthor
1410	84.5	2.1	402	1	HMP_BACAN	Q8lt23	bacillus an
1411	84.5	2.1	402	1	HMP_BACHK	Q6hla6	bacillus th
1412	84.5	2.1	402	2	Q63DT3	Q63dt3	bacillus ce
1413	84.5	2.1	419	2	Q68CR6	Q68cr6	homo sapien
1414	84.5	2.1	420	2	Q7VH00	Q7vh00	helicobacte
1415	84.5	2.1	421	2	Q6D8X3	Q6d8x3	erwinia car
1416	84.5	2.1	428	2	Q9Z5W0	Q9z5w0	pseudomonas
1417	84.5	2.1	435	2	Q6AC51	Q6ac51	leifsonia x
1418	84.5	2.1	438	2	Q6UUM5	Q6uum5	oryza sativ
1419	84.5	2.1	446	2	Q965R9	Q965r9	caenorhabdi
1420	84.5	2.1	463	2	Q6L081	Q6l081	picrophilus
1421	84.5	2.1	464	2	Q9FLV6	Q9flv6	arabidopsis
1422	84.5	2.1	471	1	Y782_SYNY3	Q55629	synechocyst
1423	84.5	2.1	475	1	IDH_SYNY3	P80046	synechocyst
1424	84.5	2.1	482	1	MUE1_CLOAB	Q97h84	clostridium
1425	84.5	2.1	489	2	Q6ESV8	Q6esv8	oryza sativ
1426	84.5	2.1	507	2	Q7V5N1	Q7v5n1	prochloroco
1427	84.5	2.1	508	2	Q8D426	Q8d426	vibrio vuln
1428	84.5	2.1	510	1	FUMH_HUMAN	P07954	homo sapien
1429	84.5	2.1	519	2	O33968	O33968	streptomyce
1430	84.5	2.1	523	2	Q8VZ53	Q8vz53	arabidopsis
1431	84.5	2.1	523	2	Q9SRQ6	Q9srq6	arabidopsis
1432	84.5	2.1	524	2	Q80UE9	Q80ue9	mus musculu
1433	84.5	2.1	530	2	Q648D8	Q648d8	uncultured
1434	84.5	2.1	550	2	Q87CQ0	Q87cq0	xylella fas
1435	84.5	2.1	555	2	Q9SPL6	Q9spl6	cichorium i
1436	84.5	2.1	561	2	Q6GZS5	Q6gzs5	frog virus
1437	84.5	2.1	580	2	Q9PPB7	Q9ppb7	campylobact
1438	84.5	2.1	582	2	Q8AB47	Q8ab47	bacteroides
1439	84.5	2.1	584	2	Q7U6E4	Q7u6e4	synechococc
1440	84.5	2.1	593	2	Q8TE67	Q8te67	homo sapien

1441	84.5	2.1	595	1	TRPE_ARATH	P32068	arabidopsis
1442	84.5	2.1	616	2	Q8N1P7	Q8nlp7	homo sapien
1443	84.5	2.1	626	2	Q9FKY0	Q9fky0	arabidopsis
1444	84.5	2.1	627	2	Q8Z978	Q8z978	salmonella
1445	84.5	2.1	639	2	Q9H9M1	Q9h9m1	homo sapien
1446	84.5	2.1	644	2	Q8W2Z9	Q8w2z9	oryza sativ
1447	84.5	2.1	655	2	Q7QEL2	Q7qel2	anopheles g
1448	84.5	2.1	663	2	Q8AW55	Q8aw55	brachydanio
1449	84.5	2.1	667	2	Q7S412	Q7s412	neurospora
1450	84.5	2.1	677	2	Q9W2G8	Q9w2g8	drosophila
1451	84.5	2.1	680	1	LRC4_MOUSE	Q921g6	mus musculu
1452	84.5	2.1	712	1	IRAI_HUMAN	P51617	homo sapien
1453	84.5	2.1	737	2	Q94706	Q94706	physarum po
1454	84.5	2.1	755	2	Q82KQ8	Q82kq8	streptomyce
1455	84.5	2.1	757	2	Q6D436	Q6d436	erwinia car
1456	84.5	2.1	760	1	MCM7_SCHPO	O75001	schizosacch
1457	84.5	2.1	769	2	Q8CGH2	Q8cgh2	mus musculu
1458	84.5	2.1	789	2	Q9EPL1	Q9ep11	mus musculu
1459	84.5	2.1	791	2	Q91S44	Q91s44	regina rana
1460	84.5	2.1	845	2	Q9WRJ9	Q9wrj9	hepatitis b
1461	84.5	2.1	862	2	Q8W4X6	Q8w4x6	prunus dulc
1462	84.5	2.1	872	2	Q9FLV4	Q9flv4	arabidopsis
1463	84.5	2.1	889	2	Q72H73	Q72h73	thermus the
1464	84.5	2.1	903	1	DPOL_BPR69	Q38087	bacterioph
1465	84.5	2.1	953	2	Q811B1	Q811b1	mus musculu
1466	84.5	2.1	963	2	Q726F3	Q726f3	desulfovibr
1467	84.5	2.1	989	2	Q6C3P4	Q6c3p4	yarrowia li
1468	84.5	2.1	996	2	Q8P9F2	Q8p9f2	xanthomonas
1469	84.5	2.1	1000	2	Q96YM3	Q96ym3	sulfolobus
1470	84.5	2.1	1011	2	Q79A30	Q79a30	bacillus li
1471	84.5	2.1	1102	2	Q8YTS0	Q8yts0	anabaena sp
1472	84.5	2.1	1142	2	Q6UVM4	Q6uvm4	rattus norv
1473	84.5	2.1	1153	2	Q8BQ40	Q8bq40	mus musculu
1474	84.5	2.1	1158	2	O97169	O97169	drosophila
1475	84.5	2.1	1183	2	Q8LRD8	Q8lrd8	oryza sativ
1476	84.5	2.1	1198	2	Q6PW37	Q6pw37	rattus norv
1477	84.5	2.1	1204	1	POL_MLVFF	P26809	friend muri
1478	84.5	2.1	1204	2	O41250	O41250	rauscher mu
1479	84.5	2.1	1288	2	Q75WB5	Q75wb5	bos taurus
1480	84.5	2.1	1288	2	O93437	O93437	gallus gall
1481	84.5	2.1	1334	2	Q8PHD6	Q8phd6	xanthomonas
1482	84.5	2.1	1346	2	Q9ZGI2	Q9zgi2	streptomyce
1483	84.5	2.1	1349	2	Q6PAN9	Q6pan9	mus musculu
1484	84.5	2.1	1440	2	Q86WJ2	Q86wj2	homo sapien
1485	84.5	2.1	1454	2	Q9X578	Q9x578	bacillus su
1486	84.5	2.1	1485	2	Q7N936	Q7n936	photorhabdu
1487	84.5	2.1	1495	2	Q9KID8	Q9kid8	streptomyce
1488	84.5	2.1	1499	2	Q9X579	Q9x579	bacillus su
1489	84.5	2.1	1518	2	Q8THT8	Q8tht8	methanosarc
1490	84.5	2.1	1555	2	Q7PPH8	Q7pph8	anopheles g
1491	84.5	2.1	1559	2	Q8YP56	Q8yp56	anabaena sp
1492	84.5	2.1	1560	2	Q7SDW7	Q7sdw7	neurospora
1493	84.5	2.1	1612	2	Q7SGM7	Q7sgm7	neurospora
1494	84.5	2.1	1734	2	Q7QB22	Q7qb22	anopheles g
1495	84.5	2.1	1743	2	Q9XWX5	Q9xwx5	caenorhabdi
1496	84.5	2.1	1972	1	P531_HUMAN	Q12888	homo sapien
1497	84.5	2.1	1977	2	Q7Z3U4	Q7z3u4	homo sapien

1498	84.5	2.1	2104	2	Q8XC75	Q8xc75 escherichia
1499	84.5	2.1	2271	2	Q9C443	Q9c443 cryptococcu
1500	84.5	2.1	3059	2	Q8BBW3	Q8bbw3 potato viru

ALIGNMENTS

RESULT 1

SM4A_HUMAN

ID SM4A_HUMAN STANDARD; PRT; 761 AA.

AC Q9H3S1; Q8WUA9;

DT 28-FEB-2003 (Rel. 41, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Semaphorin 4A precursor (Semaphorin B) (Sema B) (UNQ783/PRO1317).

GN Name=SEMA4A; Synonyms=SEMB;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Miyajima N.,

RA Saito T.;

RT "Human semaphorin B.";

RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

RA Godowski P., Gray A.;

RT "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

RT bioinformatics assessment.";

RL Genome Res. 13:2265-2270(2003).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Colon;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Inhibits axonal extension by providing local signals to
 CC specify territories inaccessible for growing axons (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; AB029394; BAB20087.1; -.
 DR EMBL; AY358531; AAQ88895.1; -.
 DR EMBL; BC020974; AAH20974.1; -.
 DR Genew; HGNC:10729; SEMA4A.
 DR H-InvDB; HIX0022447; -.
 DR MIM; 607292; -.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR PROSITE; PS51004; SEMA; 1.
 KW Developmental protein; Glycoprotein; Immunoglobulin domain;
 KW Multigene family; Neurogenesis; Signal; Transmembrane.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 761 Semaphorin 4A.
 FT DOMAIN 33 683 Extracellular (Potential).
 FT TRANSMEM 684 704 Potential.
 FT DOMAIN 705 761 Cytoplasmic (Potential).
 FT DOMAIN 36 494 Sema.
 FT DOMAIN 496 548 PSI.
 FT DOMAIN 573 631 Ig-like C2-type.
 FT DISULFID 580 624 By similarity.
 FT CARBOHYD 120 120 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 135 135 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 496 496 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 607 607 N-linked (GlcNAc . . .) (Potential).
 FT CONFLICT 293 328 CTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQW -> S
 FT APSRGSCPSTSSATRSCSPPILPQLPTSTQSSPPSG (in
 FT Ref. 1).
 FT CONFLICT 354 354 Y -> F (in Ref. 1).
 SQ SEQUENCE 761 AA; 83573 MW; 5BCB889AA32A2BB3 CRC64;

Query Match 100.0%; Score 4031; DB 1; Length 761;
Best Local Similarity 100.0%; Pred. No. 1.9e-314;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMRVRYYAGDERRALSFFHQKG	60
Db	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMRVRYYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKS	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKS	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFILMDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFILMDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTGTTGSLHKAVVSGDSSAHLVEEIQLFDPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTGTTGSLHKAVVSGDSSAHLVEEIQLFDPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAVLVSGALIIIVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAVLVSGALIIIVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 2

Q6MZT6

ID Q6MZT6 PRELIMINARY; PRT; 723 AA.
AC Q6MZT6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686D04248.
GN Name=DKFZp686D04248;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RG The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BX640891; CAE45942.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000005; HTHAraC.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 723 AA; 79708 MW; 42D7997A2B042580 CRC64;

Query Match 94.9%; Score 3827; DB 2; Length 723;
Best Local Similarity 99.9%; Pred. No. 4.3e-298;
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	39	MPRVRYAGDERRALSFFHQGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLK	98
Db	1	MPRVRYAGDERRALSFFHQGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLK	60
Qy	99	NMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQD	158
Db	61	NMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQD	120
Qy	159	SYLLPISEDKVMGKQGSPFDPAHKHHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVL	218
Db	121	SYLLPISEDKVMGKQGSPFDPAHKHHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVL	180
Qy	219	KTDNFLRWLHHDASFVAAPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKL	278
Db	181	KTDNFLRWLHHDASFVAAPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKL	240

Qy	279	LQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAV	338
Db	241	LQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAV	300
Qy	339	CAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLM	398
Db	301	CAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLM	360
Qy	399	DEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVE	458
Db	361	DEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTTPGSLHKAVVSGDSSAHLVE	420
Qy	459	EIQLFDPPEPVRNLQLAPTQGA VFGVGGVWRVPRANCSVYESCVDCVLARDPHCAWDP	518
Db	421	EIQLFDPPEPVRNLQLAPTQGA VFGVGGVWRVPRANCSVYESCVDCVLARDPHCAWDP	480
Qy	519	ESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILEL	578
Db	481	ESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILEL	540
Qy	579	PCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISY	638
Db	541	PCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISY	600
Qy	639	WVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVL FALVLSGA	698
Db	601	WVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVL FALVLSGA	660
Qy	699	LIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGT	758
Db	661	LIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGT	720
Qy	759	EVA 761	
Db	721	EVA 723	

RESULT 3

Q66HA9

ID	Q66HA9	PRELIMINARY;	PRT;	760 AA.
AC	Q66HA9;			
DT	25-OCT-2004 (TrEMBLrel. 28, Created)			
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)			
DE	Hypothetical protein.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Director MGC Project;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC081943; AAH81943.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 760 AA; 83286 MW; E97A61CD1FEBFDC5 CRC64;

Query Match 84.0%; Score 3385.5; DB 2; Length 760;
 Best Local Similarity 84.0%; Pred. No. 1.3e-262;
 Matches 639; Conservative 51; Mismatches 70; Indels 1; Gaps 1;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG	60
		: : :	
Db	1	MALPSLGQDPWSLLSVFFFQLFLLLSLPPASGTGGQGPVPRVKYHAGDGHRLSFFQQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKS	120
		:	
Db	61	LRDFDTLLLSGDGNTLYVGAREAILALNIENPGIPRLRNMIWPASEKKKNECAFKKKS	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNATHLYACGTFAFSPACTFIELQDSFLLPILKDKVTDGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Db	181	AHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDIFLRWLHPDASFVAAPST	240
Qy	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVYFFFEETASEFDFFEELYTSRVAQVCKNDVGGEKLLQKKWTTFLKAQLLCAQPGQLP	300

Db	119	SNETQCFNFIRVLVSYNATHLYACGTFFAFSPACTFIELQDSLLLPILDKVMGKGQSPL	178
Qy	179	DPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIP	238
Db	179	TLFTSTQAVLVDGMLYSGTMNFLGSEPILMRTLGSHPVLKTDIFLRWLHADASFVAAIP	238
Qy	239	STQVVYFFFEETASEFDFFERLHTRSARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ	298
Db	239	STQVVYFFFEETASEFDFFELYISRVAQVCKNDVGGEKLLQKKWTTFLKAQLLCAQPGQ	298
Qy	299	LPFNIRHAVLLPADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELN	358
Db	299	LPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELN	358
Qy	359	KETSRWTTYRGPEPNRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRL	418
Db	359	KETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRL	418
Qy	419	AVETAQGLDGSHSLVMYLGTTTGSILHKAIVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQ	478
Db	419	AVESARGLDGSSHVMYLGTTSTGPLHKAIVPDSSAYLVEEIQSPDSEPVRNLQLAPAQ	478
Qy	479	GAVFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDM	538
Db	479	GAVFAGFSGGIWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCLLSG-STKPWKQDM	537
Qy	539	ERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAV	598
Db	538	ERGNPEWVCTRGPMASSPRRQSPQLIKEVLTVPNSILELRCPHLSALASYHWSHGRAKI	597
Qy	599	PEASSTVYNGSLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPR	658
Db	598	SEASATVYNGSLLLLPQDGVGGGLYQCVATENGYSYPVVSYWVDSQDQPLALDPELAGVPR	657
Qy	659	EHVKVPLTRVSGGAALAAQSYWPHFVTVTVLFLVLSGALIILVASPLRALRARGKVQG	718
Db	658	ERVQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIVLLGVLTLLLASPLGALRARGKVQG	717
Qy	719	CETLRPGEKAPLSREQHLQSPKECRTSASDQDADNNCLGTEVA	761
Db	718	CGMLPPREKAPLSRDQHLQPSKDHRTSASDQDADNNHLGAEVA	760

RESULT 5

Q9HA40

ID Q9HA40 PRELIMINARY; PRT; 328 AA.
AC Q9HA40;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ12287.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL; AK022349; BAB14018.1; -.
 DR HSSP; Q92854; 1OLZ.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003684; F:damaged DNA binding; IEA.
 DR GO; GO:0008094; F:DNA-dependent ATPase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR GO; GO:0006281; P:DNA repair; IEA.
 DR InterPro; IPR000005; HTHAraC.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001553; RecA.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR PRINTS; PR00142; RECA.
 DR SMART; SM00423; PSI; 1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
 SQ SEQUENCE 328 AA; 35403 MW; 6F455687BFCB2312 CRC64;

Query Match

43.2%; Score 1743; DB 2; Length 328;

Best Local Similarity 100.0%; Pred. No. 2.8e-131;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      434 MYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVP 493
          |||
Db      1 MYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVP 60

Qy      494 RANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPM 553
          |||
Db      61 RANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPM 120

Qy      554 RSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAPPEASSTVYNGSLLLI 613
          |||
Db      121 RSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAPPEASSTVYNGSLLLI 180

Qy      614 VQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAA 673
          |||
Db      181 VQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAA 240

Qy      674 LAAQQSYWPHFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSRE 733
          |||
Db      241 LAAQQSYWPHFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSRE 300

Qy      734 QHLQSPKECRTSASDVDADNNCLGTEVA 761
          |||
Db      301 QHLQSPKECRTSASDVDADNNCLGTEVA 328
```

RESULT 6

Q6DCP0

ID Q6DCP0 PRELIMINARY; PRT; 835 AA.
AC Q6DCP0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Sema4b-prov protein.
GN Name=sema4b-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC077964; AAH77964.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 SQ SEQUENCE 835 AA; 94003 MW; 7E113B06741E2C80 CRC64;

Query Match 32.6%; Score 1316; DB 2; Length 835;
 Best Local Similarity 37.8%; Pred. No. 2.1e-96;
 Matches 301; Conservative 133; Mismatches 267; Indels 96; Gaps 24;

QY 11 WSLGLFLFQLLQLLLP TTTAGGGGQGPMRVRYYAGDERRALSFFHQKGLQDFDTLLLS 70
 || || | || | : :||: | | | : ||||
 Db 4 WSC--TFLVGLATLLL-----GSATEEVIPRLTLPGSPERNFKTFEADGATYYTTLLLS 56
 QY 71 GDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRV 130
 ||| ||||| : :|: | : | | : || |||| | : | |:|:
 Db 57 KDG NMLYVGARETLFSLNSTDFMSTEYHSKITWQADEEKKKECAFKGKDPQRDCQNYIKI 116
 QY 131 LVSYNVTHLYTCGTFAFSPACTFIELQDSYL-----LPISEDKVMEGKGQSPFDPAAKH 184
 |: | ||||| ||||| ||:|:| | | : || ||| : ||| :
 Db 117 LLQLNSTHLYTCGTFAFSPTCTYIKISDFSLEKNASGHPVLED----GKGRCFPDPEYNS 172
 QY 185 TAVLVDGMLYSGTMN NFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVA-----AIP 238
 ||:| ||| :|:|:| ||| |:|:| : : | : |||:| | | | :|| : :|
 Db 173 TAIMVDGEMYAGTVNNFQGNPIVYKSHESRITLKTENALYWL-QDPAFVGSAYIQESLP 231

Qy	239	STQVV-----YFFFEETASEFDDFFERLHTSRVARVCKNVDVGGEKLLQKKWTTFLKAQLL	292
Db	232	KGNLVGDDDKIYFFFFSETGKEFDFFENTIVSRIARVCKGDLGGERVLRRTWTTFLKAQLI	291
Qy	293	CTQPGQ-LPFNVIRHAVLLPADSPTAPH-----IYAVFTSQWQVGGTRSSAVCAFSLLDI	346
Db	292	CSCPGDGFPPFNVLKDMFVL---TPGEEHWKDTIFYGVFTSQWNKGGAGSSAVCAFSMDEV	348
Qy	347	ERVFKGKYKELNKETSRTWTTYRGFPETNPRPGSCSVGPSS-----DKALTFMKDH	395
Db	349	QNAENGLFKEVNRRETQQWYTYTNSVPEPRPGACITNSAKHRKINSSLHMPDRVLNFKVDH	408
Qy	396	FLMDEQVVGTPLLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAH	455
Db	409	FLMDSAIRSQPLLLQSQIRYKQISVQRVKGLK-KTYDVLFLGTDDGRLHKA-VSVNKMVH	466
Qy	456	LVEEIQLEFPDPEPVRNLQLAPTQGAVFVGFGSGGVWRVPRANCSVYESCVDCVLARDPHCA	515
Db	467	IIEEIKLFQDMQPVQELLLDPSKGLLYASSRSAAVQVPVSNCSMYRSCGECILSRDPYCA	526
Qy	516	WDPES--RTCCLLSAPNLNSWKQDMERGNPEWAC---ASGPMRSRLRP-QSRPQIIKEVL	569
Db	527	WSKKGCHRVPHHAHDPKNQHWVQDIEDANTDAHCKHNGTEAVGRAAKPNELECQKISMEL	586
Qy	570	AVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATEN	629
Db	587	NPANT---LPCKLLSNLASRVWLHNGKEIDSSYFVLPSGDLILVGSPDRAGTYECWSVEE	643
Qy	630	GFSYPVISYWVDSQD-----QTLALDPELAGIPREHVKVPLTRVSGG-----AALAA	676
Db	644	DFRKLMMRYCVGAQEGIKATTQRTETERLFPKFSVI--ENI-VNASSVSSSSSESHSAKLT	700
Qy	677	QQSYWPHFVTVTVLFA--LVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQ	734
Db	701	GKSYWMEFVIMSTLFGVMVILGLLLLY-----RNRKEMKTILKPAEHS-----	745
Qy	735	HLQSPKECRTSASDVDA	751
Db	746	--KPPKKLRKNGMPAES	760

RESULT 7

```
ID      Q6UXE3      PRELIMINARY;      PRT;      837 AA.
AC      Q6UXE3;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Semaphorin C (Semaphorin 4b precursor).
GN      Name=SEMA4B; ORFNames=UNQ749;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
```

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA White J.R., Levinson N., Lee S.R., Myers K.A., Harris R.A.,
 RA Balkwill F., Beard G.L., Naylor S.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY358392; AAQ88758.1; -.
 DR EMBL; AY445887; AAR15707.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal.
 FT SIGNAL 1 37 Potential.
 FT CHAIN 38 837 semaphorin 4b.
 SQ SEQUENCE 837 AA; 92749 MW; 2B29FCBAE68A1E21 CRC64;

Query Match 31.6%; Score 1274; DB 2; Length 837;
 Best Local Similarity 38.9%; Pred. No. 4.9e-93;
 Matches 308; Conservative 127; Mismatches 277; Indels 80; Gaps 28;

Qy 1 MALPALGL-----DPWSLL----GLFLFQLLQLLL---PTTTAGGGGQGPMRVRYYAGD 48
 | | :|| | | | | | | | | | | | | | : |
 Db 1 MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPTWA-----LSPRISLPLGS 54
 Qy 49 ERRALSFFHQGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP--RLKNMIPWPAS 106
 | | | : : : : | | | | | | | | : | : : | |
 Db 55 EERPFLRFEAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELL-WGAD 113
 Qy 107 DRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISE 166
 | | :||| | : | | :||: : : :||:| | | | | | : : | :
 Db 114 AEKKQQCSFKGKDPQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEK 173
 Qy 167 DKVM--EGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFL 224
 | : :||: | | | | | | :||| | :||: : | : | : | : |
 Db 174 GNVLLEDGKGRCFPDPNFKSTALVVDGELYTGTVSSFQGNDDPAISRSQSLRPT-KTESSL 232
 Qy 225 RWLHHDAFVAA--IPST-----QVYFFFEETASEFDFFERLHTSRVARVCKNDVG 274
 | | | :||: | | : :||| | | | :||| | | :||:| | |

Db 233 NWL-QDPAFVASAYIPESLGS LQGGDDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEG 291

Qy 275 GEKLLQKKWTTFLKAQLLCTQPGQ-LPFNVIRHAVLLPADSPTAPH-----IYAVFTSQW 328
 ||::||::||::||| |||::| | | | |

Db 292 GERV LQQRWTSFLKAQLLCSR PDDGFPFNV LQDVFTL---SPSPQDWRDTLFYGVFTSQW 348

Qy 329 QVGGRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRG PETNPRPGSCSVGPS----- 384
 | | | | | |::|::| | | | | |::| | | | | |::| | | | |

Db 349 HRGTTEGSAVCVFTMKDVQRVFSGLYKEVNRETQQWYTVTHPVPTPRPGACITNSARERK 408

Qy 385 -----SDKALTFMKDHF LMDQVVGTPLLVKSGVEYTRLAVETAQGLDGHS LVMYLG 437
 |: | |::| | | | | | | | |::| | | | | | | | |::| | | | |

Db 409 INSSLQLPDRVLNFLKDHF LMDGQVRSRMLLLQPQARYQRVAVHRVPGLH-HTYDVLFLG 467

Qy 438 TTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA VFGVFGSGGVWRVPRANC 497
 | | | | | | | |::| | | | | |::| | | | | |::| | | | |

Db 468 TGDGRLHKAVSVG-PRVHII EELQIFSSGQPQNLLDTHRGLLYAASHSGVVQVPMANC 526

Qy 498 SVYESCVDCVLARDPHCAWD PESRTCCLLSAPNL--NSWKQDMERGNPEWAC-ASGPMSR 554
 |::| | | |::| | | | | | | | |::| | | | | | | | |::| | | | |

Db 527 SLYRSCGDCLLARDPYCAWSGSSCKHVS LYPQLATRPWIQDIEGASAKDLCSASSVVP 586

Qy 555 SLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYW SHGPAAVPEASS--TVYNGSLLL 612
 | | : ::| |::| | | | | |::| | | | | |::| | | | |

Db 587 SFVPTGE-KPCEQVQFQPN TVNTLACPLLSNLATRLWL RLGAPVNASASCHVLPTGDLLL 645

Qy 613 IVQDGVGG LYGQWATENGFSYPVISYWVDSQDQTLALDPELAG-IPREHKVPLTRVS-- 669
 : : | : | | | | | | | | : : | : | : | | | : | |

Db 646 VGTQQLGE-FQCWSLEEGFQQLVAS YCPEVVEDGVADQTDEGGSVP----VIISTSRVSAP 701

Qy 670 --GGAALAAQSYWPHFVTVTVLFAL-VLSGALII LV--ASPLRALRARGKV-----QGC 719
 | | : | : | | | : : | | | | | : | : : : | : : |

Db 702 AGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFL LLYRHRNSMKVFLKQGE CASVHPKTC 761

Qy 720 ETLRPGEKAPLS 731
 : | | | |

Db 762 PVLPPETRPLN 773

RESULT 8

SM4B_HUMAN

ID SM4B_HUMAN STANDARD; PRT; 832 AA.

AC Q9NPR2; Q8WVP9; Q96FK5; Q9C0B8; Q9H691; Q9NPM8; Q9NPN0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Semaphorin 4B precursor.

GN Name=SEMA4B; Synonyms=KIAA1745;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=21082932; PubMed=11214970;

RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XIX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:347-355(2000).
RN [2]
RP SEQUENCE OF 160-832 FROM N.A., AND VARIANT ALA-792.
RA Carim L., Estivill X., Escarceller M., Sumoy L.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 358-832 FROM N.A.
RX PubMed=14702039; DOI=10.1038/ngl285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [4]
RP SEQUENCE OF 303-832 FROM N.A., AND VARIANT ALA-792.
RC TISSUE=Colon, and Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 39-53.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 CC -!- FUNCTION: Inhibits axonal extension by providing local signals to
 CC specify territories inaccessible for growing axons (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to a
 CC frameshift in position 709.
 CC -----
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 CC -----
 DR EMBL; AB051532; BAB21836.1; -.
 DR EMBL; AL390080; CAB98204.1; -.
 DR EMBL; AL390081; CAB98205.1; -.
 DR EMBL; AL390082; CAB98206.1; -.
 DR EMBL; AK026133; BAB15372.1; ALT_FRAME.
 DR EMBL; BC010701; AAH10701.1; ALT_INIT.
 DR EMBL; BC017658; AAH17658.1; -.
 DR Genew; HGNC:10730; SEMA4B.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS51004; SEMA; 1.
 KW Developmental protein; Direct protein sequencing; Glycoprotein;
 KW Immunoglobulin domain; Multigene family; Neurogenesis; Polymorphism;
 KW Signal; Transmembrane.
 FT SIGNAL 1 38
 FT CHAIN 39 832 Semaphorin 4B.
 FT DOMAIN 39 712 Extracellular (Potential).
 FT TRANSMEM 713 733 Potential.

Qy 512 PHCAWDPE\$RTCCLL\$APNL--NSWKQD\$MERGN\$PEWAC-ASGPM\$SRSLRPQ\$SRPQIIKEV 568
 |::|| | | | | |::| : : | | : | | : : |
 Db 536 PYCAWSG\$SSCKHVS\$LYQPQLATRPWIQDIEGASAKDLCSASSV\$VSP\$SFVPTGE-KPCEQV 594

Qy 569 LAVPNSILELPCPHLSALASYW\$SHGPA\$AVPEASS--TVYNG\$SLLLIVQDGVGGLYQCWA 626
 ||:: | || || ||: | | | : | ||: : | : ||:
 Db 595 QFQPNTVNTLACPLLSNLATRLWLRNGAPVNASASCHVLP\$TGDLLL\$VGTQQLGE-FQCWS 653

Qy 627 TENGFSYPVISYWVDSQDQTLALDPELAG-IPREHV\$KVPLTRVS----GGAALAAQ\$QSYW 681
 | || | || : : : | : | : | | : : || | | : | : ||
 Db 654 LEEGFQQLVASYCPEVVEDGVADQTDEGGSVP---VIISTSRVSAPAGGKASWGADRSYW 710

Qy 682 PHFVTVTVLFAL-VLSGALIILV--ASPLRALRARGKV-----QGCE\$TLRPGEKAPLS 731
 | : : || | || | : | : : : | : : | : | | ||:
 Db 711 KEFLVMCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGE\$CASVHPKTC\$PVVLP\$PETRPLN 768

RESULT 9

Q69ZB7

ID Q69ZB7 PRELIMINARY; PRT; 871 AA.
 AC Q69ZB7;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE MKIAA1745 protein (Fragment).
 GN Name=mKIAA1745;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
 RA Nagase T., Ohara O., Koga H.;
 RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
 RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
 RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
 RT Randomly Sampled from Size-Fractionated Libraries.";
 RL DNA Res. 11:205-218(2004).
 DR EMBL; AK173249; BAD32527.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR000005; HTHAraC.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR011047; Quin_alc_DH_like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
 FT NON TER 1 1
 SQ SEQUENCE 871 AA; 96449 MW; A84E4A30B87452B9 CRC64;

Query Match 30.9%; Score 1246.5; DB 2; Length 871;
 Best Local Similarity 39.5%; Pred. No. 8.4e-91;
 Matches 294; Conservative 118; Mismatches 264; Indels 69; Gaps 24;

Qy	3	LPALGLDPWSLLG-----LFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRA	52
		: :	
Db	38	LPAAVRAPRAAMGRASRAVLRRALLLLLLLLLLLRTTTTRALG----PRISVPLGSEERL	93
Qy	53	LSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP--RLKNMIPWPASDRKK	110
		: : : : : : : : :	
Db	94	IRKFEAENISNYTALLSQDGKTLVGAREALFALNSNLSFLPGGEYQELL-WSADADRK	152
Qy	111	SECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVM	170
		: : : : : : : : :	
Db	153	QQCSFKGKDPKRDCQNYIKILLPLNSSHLLTCGTAAFSPLCAYIHIASTLAQDEAGNVI	212
Qy	171	--EGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLH	228
		: : : : : :	
Db	213	LEDGKGRCFPDPNFKSTALVVDGELYTGTVSSFGQNDPAISRSQSSRPT-KTESSLNWL-	270
Qy	229	HDASFVAA-----IPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKL	278
		: : :	
Db	271	QDPAFVASAYVPESLGSPIGDDDKIYFFFSETGQFEFFENTIVSRVARVCKGDEGGERV	330
Qy	279	LQKKWTTFLKAQLLCTQPGQ-LPFNVIRHAVLL---PADSPTAPHIYAVFTSQWQVGGTR	334
		: : : :	
Db	331	LQQRWTSFLKAQLLCSRPDGFPFNVLQDVFTLNPNPQDW-RKTLFYGVFTSQWHRGTTE	389
Qy	335	SSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPS-----	384
		: : : : : :	
Db	390	GSAICVFTMNDVQKAFDGLYKKVNRETQQWYTETHQVPTPRGACITNSARERKINSSLQ	449
Qy	385	-SDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHS-HLVMYLGTTTGS	442
		: : : : :	
Db	450	LPDRVLNFLKDHFLMDGQVRSRLLLQPRARYQRVAVHRVPGL--HSTYDVLFGLTGDGR	507
Qy	443	LHKAVVSGDSSAHLVEEIQLPDPEPVRLQLAPTQGAVFVGFSGGVWRVPRANCSVYES	502
		: : : : : : : : :	
Db	508	LHKAVTL-SSRVHIIIEELQIFPQGQPVQNLLDSHGGLLYASSHSGVVQVPVANCSTLYPT	566
Qy	503	CVDCVLARDPHCAWDPESTRCCLLSAPNLNS--WKQDMERGNPEWACASGPMSRSLRPQS	560
		: : : : :	
Db	567	CGDCLLARDPYCAWTGSACRLASLYQPDLASRPWTQDIEGASVKELCKNSSYKARFLVPG	626
Qy	561	RPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASS--TVYNGSLLLI-VQDG	617
		: : : : : : :	
Db	627	KP--CKQVQIQPNTVNTLACPLLSNLATRLWVHNGAPVNASASCRVLPDGLLLVGSQQG	684
Qy	618	VGGLYQCWATENGFSYPVISYWVDSQDQ-TLALDPELAGIPREHVKVPLTRVS-----GGA	672
		: : : : : : : : :	
Db	685	L-GVFQCWSIEEGFQQQLVASYCPEVMEEGVMDQKNQRDGTGTP---VIINTSRVSAPAGGRA	740
Qy	673	ALAAQQSYWPHFVTVTVL--FALVL	695
		: : : :	
Db	741	SWGADKSYWNEFLVMCTLFVFAMVL	765

RESULT 10

Q8BIR6

ID Q8BIR6 PRELIMINARY; PRT; 823 AA.
AC Q8BIR6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
DE RIKEN full-length enriched library, clone:5031439F07
DE product:SEMAPHORIN 4B (SEMAPHORIN C) (SEMA C), full insert
DE sequence.
GN Name=Sema4b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/350555500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK030331; BAC26906.1; -.
 DR HSSP; Q92854; 1OLZ.
 DR MGD; MGI:107559; Sema4b.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR000005; HTHAraC.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
 SQ SEQUENCE 823 AA; 91485 MW; E3B8C5E5CFA1CD45 CRC64;

Query Match 30.7%; Score 1239.5; DB 2; Length 823;
 Best Local Similarity 37.6%; Pred. No. 2.8e-90;
 Matches 295; Conservative 128; Mismatches 289; Indels 73; Gaps 24;

Qy 13 LLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDTLLLSGD 72
 || | : || || ||| | ||: : | : | : : : |||| |
 Db 11 LLSIMVLLLLLLLLLWTTTTRALG-----PRINVPLCCQERLIRKFEAENISNYTALLLSQD 65
 Qy 73 GNTLYVGAREAILALDIQDPGVP--RLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRV 130
 | ||||| ||| : ||: : | : : | | : | : || | : | ||: :
 Db 66 GKTLYVGAREALFALNSNLSFLPGGEYQELL-WSADADRKQQCSFKGKDPKRDCQNYIKI 124
 Qy 131 LVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVM--EGKGQSPFDPAHKHTAVL 188
 | : | : || |||| |||| | : | : | : : ||| : |||| | ||: :
 Db 125 LLPLNSSHLLTCGTAAFSPLCAYIHIASTLAQDEAGNVILEDGKGRCFPDPNFKSTALV 184
 Qy 189 VDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAA-----IP 238
 ||| ||: ||: : | ||: | : | : | ||: | || | : ||| : |
 Db 185 VDGElyTGTVSSFQGNdPAISRSQSSRPT-KTESSLNWL-QDPAFVASAYVPESLGSPIG 242

Qy 239 STQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGKLLQKKWTTFLKAQLLCTQPGQ 298
 :||| || ||:| | ||||| | ||::||::||:|||||||::|
 Db 243 DDDRIYFFFSETGQFEFFENTIVSRVARVCKGDEGGERVLQQRWTSFLKAQLLCSRDD 302

Qy 299 -LPFNVRHAVLL---PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKY 354
 |||:: | | | | |||| | | ||:| |: |:: | | |
 Db 303 GFPFNVLQDVFTLNPNPQDW-RKTLFYGVFTSQWHRGTTEGSAICVFTMNDVQKAFDGLY 361

Qy 355 KELNKETSRWTTYRGPETNPRPGSCSVGPS-----SDKALTFMKDHFMLDEQVV 403
 |::||| :| | ||||: | : | | | |||| | |
 Db 362 KKVNRQTQQWYTETHQVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFMLDQGVR 421

Qy 404 GTPLLKSGVEYTRLAVETAQGLDGHS-HLVMYLGTGSLHKAVVSGDSSAHLVEEIQ 462
 ||:: | |::| | | : |::|| | |||| | |::||:|
 Db 422 SRLLLQPRARYQRVAVHRVPG--HSTYDVLFLGTGDGRLHKAVTL-SSRVHIEELQI 478

Qy 463 FPDPEPVRNLQLAPTQGAFFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE 522
 || :||:| | | : | | :|| ||||:| :| ||:||||:| | :
 Db 479 FPQGGPVQNLLDLSHGGLLYASSHSGVVQVPVANCPLYPTCGDCLLARDPYCAWTGSACR 538

Qy 523 CCLLSAPNLNS--WKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPC 580
 | |::| | ||:| : : | : :| |:: | |
 Db 539 LASLYKPDLASRPWTQDIEGASVKELCKNSSYKARFLVPGKP--CKQVQIQPNTVNTLAC 596

Qy 581 PHLSALASYWYSHGPAAPVEASS--TVYNGSLLLI-VQDGVGGLYQCWATENGFSYPVIS 637
 | || ||: | | | | :| : | ||: | | :||:| | | | |
 Db 597 PLLSNLATRLWVHNGAPVNASASCRVLPDGLLLVGSQQGL-GVFQCWSIEEGFQQLVAS 655

Qy 638 YWVDSQDQ-TLALDPELAGIPREHVKVPLTRVS----GGAALAAQQSYWPHFVTVTVLFA 692
 | : :: : | | | : :|| | | : | :|| | : : ||
 Db 656 YCPEVMEEGVMDQKNQRDGTP---VIINTSRVSAPAGGRASWGADKSYWNEFLVMCTLFV 712

Qy 693 LVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASD 752
 : : | : : | | : | : : | | |
 Db 713 FAMVLLFLFLLYRHRDGMKFLKQGECAVHP-----KTRPIVLPPEPTRPL----- 758

Qy 753 NNCLG 757
 ||:|
 Db 759 -NCVG 762

RESULT 11

SM4B_MOUSE

ID SM4B_MOUSE STANDARD; PRT; 782 AA.
 AC Q62179;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Semaphorin 4B (Semaphorin C) (Sema C) (Fragment).
 GN Name=Sema4b; Synonyms=SEMAC, SemC;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Brain;

RX MEDLINE=95267431; PubMed=7748561; DOI=10.1016/0896-6273(95)90332-1;
 RA Pueschel A.W., Adams R.H., Betz H.;
 RT "Murine semaphorin D/collapsin is a member of a diverse gene family
 RT and creates domains inhibitory for axonal extension.";
 RL Neuron 14:941-948(1995).
 RN [2]
 RP INTERACTION WITH GIPC.
 RX MEDLINE=99253973; PubMed=10318831; DOI=10.1074/jbc.274.20.14137;
 RA Wang L.-H., Kalb R.G., Strittmatter S.M.;
 RT "A PDZ protein regulates the distribution of the transmembrane
 RT semaphorin, M-SemF.";
 RL J. Biol. Chem. 274:14137-14146(1999).
 CC -!- FUNCTION: Inhibits axonal extension by providing local signals to
 CC specify territories inaccessible for growing axons.
 CC -!- SUBUNIT: Interacts with GIPC PDZ domain.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DEVELOPMENTAL STAGE: Expressed from day 10 in the embryo. Low
 CC levels found between days 10-12. Expression peaks on day 13 with
 CC moderate levels from then until birth.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X85992; CAA59984.1; -.
 DR PIR; I48746; I48746.
 DR MGD; MGI:107559; Sema4b.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS51004; SEMA; 1.
 KW Developmental protein; Glycoprotein; Immunoglobulin domain;
 KW Multigene family; Neurogenesis; Transmembrane.
 FT NON_TER 1 1
 FT DOMAIN <1 662 Extracellular (Potential).
 FT TRANSMEM 663 683 Potential.
 FT DOMAIN 684 782 Cytoplasmic (Potential).
 FT DOMAIN <1 469 Sema.
 FT DOMAIN 471 525 PSI.
 FT DOMAIN 548 608 Ig-like C2-type.
 FT DOMAIN 703 726 Pro-rich.
 FT DISULFID 555 601 By similarity.
 FT CARBOHYD 12 12 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 15 15 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 42 42 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 88 88 N-linked (GlcNAc. . .) (Potential).

FT	CARBOHYD	356	356	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	471	471	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	526	526	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	574	574	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	639	639	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	782 AA; 86823 MW; 627A81FC8F8F7AC8 CRC64;		

Query Match 29.7%; Score 1198.5; DB 1; Length 782;
 Best Local Similarity 39.9%; Pred. No. 5.1e-87;
 Matches 275; Conservative 115; Mismatches 244; Indels 55; Gaps 22;

Qy	49	ERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP--RLKNMIPWPAS	106
		: : : : : : :	
Db	1	EERLIRKFEAENISNYTALLSQDGKTLVVGAREALFALNSNLSFLPGGEYQELL-WSAD	59
Qy	107	DRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISE	166
		: : : : : : : : : :	
Db	60	ADRKQQCSFKGKDPKRDCQNYIKILLPLNSSHLITCGTAAFSPLCAYIHIASTLAQDEA	119
Qy	167	DKVM--EGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFL	224
		: : : : : : : : :	
Db	120	GNVILEDGKGHCPCFDPNFKSTALVVDGELYGTGVSSFQGNDAISRSQSSRPT-KTESSL	178
Qy	225	RWLHHDASFVAAPSTQ-----VYFFFEETASEFDFFERLHTSRVARVCKNDVG	274
		: : : : : :	
Db	179	NWL-QDPAFVASATSPESLGSPIGDDDKIYFFSETGQEFEFFENTIVSRVARVCKGDEG	237
Qy	275	GEKLLQKKWTTFLKAQLLCTQPGQ-LPFNVIRHAVLL---PADSPTAPIYAVFTSQWQV	330
		: : : : : :	
Db	238	GERVLQQRWTSFLKAQLLCSRPDGFPFNVLQDVFTLNPNPQDWRKTLGI-GVFTSQWHR	296
Qy	331	GGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPS-----	384
		: : : : : : : : :	
Db	297	GTTEGSAICVFTMNDVQKAFDGLYKKVNRETQQWYTETHQVPTPRPGACITNSARERKIN	356
Qy	385	-----SDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHS-HLVMYLGT	438
		: : : : : : :	
Db	357	SSLQLPDRVLNFKDHFLMDGQVRSRLLLQPRARYQRVAVHRVPGI--HSTYDVLFGLT	414
Qy	439	TTGSLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCS	498
		: : : : : : :	
Db	415	GDGRHLKAVTL-SSRVHIIIEELQIFPQGGPVQNLLDSHGGLLYASSHSGVVQVPVANCS	473
Qy	499	VYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNS--WKQDMERGNPEWACASGPMSRSL	556
		: : : : : : : :	
Db	474	LYPTCGDCLLARDPYCAWTGSACRLASLYQPDLASRPWTQDIEGASVKELCKNSSYKARF	533
Qy	557	RPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASS--TVYNGSLLLI-	613
		: : : : : : :	
Db	534	LVPGKP--CKQVQIQPNTVNTLACPLLSNLATRLVWHNGAPVNASASCRVLPDGLLLVG	591
Qy	614	VQDGVGGLYQCWATENGFSYPVISYWVDSQDQ-TLALDPELAGIPREHVKVPLTRVS---	669
		: : : : : : : : :	
Db	592	SQQGL-GVFQCWSIEEGFQQQLVASYCPEVMEEGVMDQKNQRDGTGTP---VIINTSRVSAPA	647
Qy	670	-GGAALAAQQSYWPHFVTVTVL--FALVL	695
		: : : : :	

RESULT 12

Q6DCD2

ID Q6DCD2 PRELIMINARY; PRT; 834 AA.
AC Q6DCD2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS *Xenopus laevis* (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; *Xenopus*.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC078116; AAH78116.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 834 AA; 93090 MW; 469A3B70AF639466 CRC64;

Query Match 27.3%; Score 1099; DB 2; Length 834;
 Best Local Similarity 35.5%; Pred. No. 5.5e-79;
 Matches 274; Conservative 126; Mismatches 280; Indels 92; Gaps 25;

Qy	19	FQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDTLLLSGDGNTLYV	78
		: : : : :	
Db	6	FFVLALLL-RAEAWEWGLTPRKTVRYHGVSEVR--QSWH-SGVSQVMTLTLDENRGALYV	61
Qy	79	GAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTH	138
		: : : : : : :	
Db	62	GAREVIFSLDLNNG-KELRPPIWEAPADKKLECAQKGKSNQTECFNYIRFLEQFNQTH	120
Qy	139	LYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTM	198
		: : : : : : : ::	
Db	121	LVTCGTYAFQPKCAYIELSD---FTLDAENLEEGKGKVPYDPAKGHTGLILDGALYSATM	177
Qy	199	NNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFV--AAIPST-----QVYFFFE	248
		: : : : : : :: : : :	
Db	178	NNFLGTEPVIQRIVGQHNLKTEYLASWL-NEPNEVSSAHIPESVGSEIGDDDKIYFFFT	236
Qy	249	ETASEFDFFERLHTSRVARVCKNDVGGKLLQKKWTTFLKAQLLCTQPG-QLPFNVIRHA	307
		: : : : : : : : :::	
Db	237	ERALEYDCQSEQVVSRRVARICKGDLGGARTLQRKWSFLKARLLCSIPELQLNFNLLKSV	296
Qy	308	VLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTY	367
		: : : : : : : :::	
Db	297	FKLEAKEWRSTHFYAAFQARW--GDSPVSAICQYSIQDIQKVFDGPYKEYREQSQKWGRY	354
Qy	368	RGPETNPRPGSC-----SVGPSSDKALTFMKDHFLMDEQVVGVT---PLLVKSGV	413
		: : : : :	
Db	355	SDSVSPRPGSCVTNWHRNHGVSLSLELPDNTLNFVKKHPLMDDSMSTHMRPLLVRGA	414
Qy	414	EYTRLAVETAQGLDGHSHLVMYLGTGTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQ	473
		: : : : :::: : : : : : :	
Db	415	NFTTIAVQRTLGLDREPYDILFIGTENGWVNKAVSFG-STVHIIIEELQVFDKSYPVHSLA	473
Qy	474	LAPTQGAVFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNS	533
		: : : : :: : : : :	
Db	474	LSARKSLLFVGSQGLVQLPFADCSKYRSCADCILARDPYCAWNINITRCVRADQRYRPI	533
Qy	534	WKQDMERGNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSH	593


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      ||:: : : :      :::|      :| :      : : |||      | ||      | :
Db      534 LLQDIK--DSDTSVCEVQSQKAVKP-----FVKNITVGIGTNVVLPCQLSSNLAQPVWTF 586
Qy      594 GPAAV--PEASSTVYNGSLLLIVQDGVG----GLYQCWATENGFSYPVISYWVDSQDQTL 647
      : : | :: :| :| |||      | | |:: | |      || :      | :
Db      587 NGQDLESDQDDSVLFDTTLQALVILGVGTHHSGCYVCYSEEQGTQLTAESYQL-----TV 641
Qy      648 ALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAVLVSLGALIILVASPL 707
      | |      : | |      | : | | | : | || : |
Db      642 VASPSLI-----LESRAPLDGLGLVW---MMVIALGAVCL--ALFLAVVYLR 683
Qy      708 RALRARGKVQGCETLRPGEKA-----PLSREQHLQSPKECRTSASDVDAD 752
      | | :      : | | | :      | :      : : || | ||      | : |
Db      684 RKLK-----DELEKGSKSMEN TLVYPIKLPSQPKTPK-CLPSA---DSD 723

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RESULT 13

SM4C_HUMAN

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ID      SM4C_HUMAN      STANDARD;      PRT;      833 AA.
AC      Q9C0C4; Q7Z5X0;
DT      05-JUL-2004 (Rel. 44, Created)
DT      05-JUL-2004 (Rel. 44, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Semaphorin 4C precursor (UNQ5855/PRO34487).
GN      Name=SEMA4C; Synonyms=KIAA1739;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA      Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA      Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA      Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA      Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA      Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA      Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA      Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA      Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA      Godowski P., Gray A.;
RT      "The secreted protein discovery initiative (SPDI), a large-scale
RT      effort to identify novel human secreted and transmembrane proteins: a
RT      bioinformatics assessment.";
RL      Genome Res. 13:2265-2270(2003).
RN      [2]
RP      SEQUENCE OF 37-833 FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=21082932; PubMed=11214970;
RA      Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT      "Prediction of the coding sequences of unidentified human genes. XIX.
RT      The complete sequences of 100 new cDNA clones from brain which code
RT      for large proteins in vitro.";
RL      DNA Res. 7:347-355(2000).
RN      [3]
RP      SEQUENCE OF 189-833 FROM N.A.
RC      TISSUE=Muscle;

```

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBUNIT: Interacts with GIPC PDZ domain (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 CC -----
 DR EMBL; AY358842; AAQ89201.1; -.
 DR EMBL; AB051526; BAB21830.1; -.
 DR EMBL; BC017476; AAH17476.2; -.
 DR Genew; HGNC:10731; SEMA4C.
 DR MIM; 604462; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS51004; SEMA; 1.
 KW Developmental protein; Glycoprotein; Immunoglobulin domain;
 KW Multigene family; Neurogenesis; Signal; Transmembrane.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 833 Semaphorin 4C.
 FT DOMAIN 21 663 Extracellular (Potential).

FT	TRANSMEM	664	684	Potential.
FT	DOMAIN	685	833	Cytoplasmic (Potential).
FT	DOMAIN	30	497	Sema.
FT	DOMAIN	499	551	PSI.
FT	DOMAIN	556	644	Ig-like C2-type.
FT	DOMAIN	708	773	Pro-rich.
FT	CARBOHYD	106	106	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	121	121	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	310	310	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	419	419	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	522	522	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	564	564	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	602	602	S -> T (in Ref. 1).
SQ	SEQUENCE	833 AA;	92622 MW;	075FDC0A392F0CE3 CRC64;

Query Match 27.0%; Score 1090; DB 1; Length 833;
 Best Local Similarity 37.1%; Pred. No. 2.9e-78;
 Matches 275; Conservative 105; Mismatches 271; Indels 90; Gaps 24;

Qy	39	MPRVRYAGDERRALSFFHQKGLQDFD	TTTTLLSGDGNTLYVGAREAILALDIQDPGVPRLK	98
		: : : : :	: : : :	
Db	28	VPRKTVSSGELATVVRFSQTGIQDFLT	LTLTLEPTGLLYVGAREALFAFSME---	ALELQ 84
Qy	99	NMIPWPASDRKKSECAFKKKSNETQCFN	FIRVLVSYNVTHLYTCGTFAFSPACTFIELQD	158
		: : :	: : : : :	
Db	85	GAISWEAPVEKKTECIQKGKNNQTECFN	FIRFLQPYNASHLYVCGTYAFQPKCTYVNM--	142
Qy	159	SYLLPISEDKVMEGKGQSPFDPAHKHTA	VLVDGMLYSGTMNFLGSEPILMRTLGSQPVL	218
		: : : : : :	: : : : :	
Db	143	-LFTTLEHGEFEDGKGKCPYDPAKGHAG	LLVDGELYSATLNNFLGTEPIILRNMGPHSM	201
Qy	219	KTDNFLRWLHHDASFV--AAIPST-----	QVYFFFEETASEFDFFERLHTSRVARV	268
		: : : : :	: :	
Db	202	KTEYLAFWL-NEPHFVGSAYVPESVGSFT	GDDDKVYFFFRERAVESDCYAEQVVARVARV	260
Qy	269	CKNDVGGEKLLQKKWTTFLKAQLLCTQPG	-QLPFNVIRHAVLLPADSPTAPIYAVFTSQ	327
		: : : : :	: : : :	
Db	261	CKGDMGGARTLQRKWTTFLKARLACSAPN	WQLYFNQLQAMHTLQDTSWHNTTFFGVFQAQ	320
Qy	328	WQVGGRSSAVCAFSLLDIERVFKGKYKEL	NKETSRTWTTYRGPETNPRPGSC-----	379
		: : : : : :	: :	
Db	321	W--GDMYLSAICEYQLEEIQRVFEGPYKEY	HEEAQKWDRYTDPVPSRPGSCINNWHRRH	378
Qy	380	---SVGPSSDKALTFMKDHFLMDEQV---	VGTPLLVKSGVEYTRLAVETAQGLDGHSHLV	433
		: :	: : : :	
Db	379	GYTSSLELPDNIILNFVKKHPLMEEQVG	PRWSRPLLVKKGTNFTHLVADRVTGLDGATYTV	438
Qy	434	MYLGTTTGSLSLHKAVVSGDSSAHLVEEI	QLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVP	493
		: : : : :	: : : : :	
Db	439	LFIGTGDGWLKAVSLG-PWVHLIEELQLF	-DQEPMRSLVLSQSKLLFAGSRSQLVQLP	496
Qy	494	RANCSVYESCVDCVLARDPHCAWDPE	SRTCCLLSAPNLNSWKQDMERGNPEWAC-ASGPM	552
		: : : : :	: : : :	
Db	497	VADCMKYRSCADCVLARDPYCAWSVNTS	RCAVGGHSGSLLIQHVMSTSDTSGICNLRG--	554
Qy	553	SRSRLRPQSRPQIIKEVLAVPNSILELPC	PHLSA-LASYWWSHGPAAVP--EASSTVYNGS	609
		: : : :	: : : : :	

```

Db      555 SKKVRPTP-----KNITVVAGTDLVLPCHLSSNLAHARWTFGGRDLPAEQPGSFLYDAR 608
Qy      610 LLLIV----QDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPL 665
      | :| | | | :| | | | : | : | |
Db      609 LQALVMAAQPRHAGAYHCFSEEQG-----ARLAAEGYLAV-----VAGPS 650
Qy      666 TRVSGGAALAAQQSYWPHFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCETLRPG 725
      : | | | | : | | | : | | | | | | | | | |
Db      651 VTLEARAPLENLGLVW---LAVVALGAVCL--VLLLLVLSLRRRLR-----EELEKG 697
Qy      726 EKA-----PLSREQHLQSP 739
      || | | : ||
Db      698 AKATERTLVYPLELPKEPTSP 718

```

RESULT 14

SM4C_MOUSE

```

ID      SM4C_MOUSE      STANDARD;      PRT;      834 AA.
AC      Q64151;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Semaphorin 4C precursor (Semaphorin I) (Sema I) (Semaphorin C-like 1)
DE      (M-Sema F).
GN      Name=Sema4c; Synonyms=Semacl1, SEMAI;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Neonatal brain;
RX      MEDLINE=95385809; PubMed=7656991; DOI=10.1016/0014-5793(95)00850-9;
RA      Inagaki S., Furuyama T., Iwahashi Y.;
RT      "Identification of a member of mouse semaphorin family.";
RL      FEBS Lett. 370:269-272(1995).
RN      [2]
RP      INTERACTION WITH GIPC.
RX      MEDLINE=99253973; PubMed=10318831; DOI=10.1074/jbc.274.20.14137;
RA      Wang L.-H., Kalb R.G., Strittmatter S.M.;
RT      "A PDZ protein regulates the distribution of the transmembrane
RT      semaphorin, M-SemF.";
RL      J. Biol. Chem. 274:14137-14146(1999).
CC      -!- SUBUNIT: Interacts with GIPC PDZ domain.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- TISSUE SPECIFICITY: Expressed widely in the nervous tissues during
CC      development. Predominantly in the developing brain and spinal
CC      cord.
CC      -!- SIMILARITY: Belongs to the semaphorin family.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC      -!- SIMILARITY: Contains 1 Sema domain.
CC      -----
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DR EMBL; S79463; AAB35184.1; -.
DR PIR; S66498; S66498.
DR MGD; MGI:109252; Sema4c.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS51004; SEMA; 1.
KW Developmental protein; Glycoprotein; Immunoglobulin domain;
KW Multigene family; Neurogenesis; Signal; Transmembrane.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 834 Semaphorin 4C.
FT DOMAIN 21 664 Extracellular (Potential).
FT TRANSMEM 665 685 Potential.
FT DOMAIN 686 834 Cytoplasmic (Potential).
FT DOMAIN 30 497 Sema.
FT DOMAIN 499 552 PSI.
FT DOMAIN 557 645 Ig-like C2-type.
FT DOMAIN 678 687 Poly-Leu.
FT DOMAIN 709 774 Pro-rich.
FT DOMAIN 831 834 Binds to GIPC.
FT DISULFID 578 628 By similarity.
FT CARBOHYD 106 106 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 121 121 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 310 310 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 419 419 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 522 522 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 565 565 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 834 AA; 92556 MW; 6868BB5BF571482D CRC64;

Query Match 26.8%; Score 1079.5; DB 1; Length 834;

Best Local Similarity 35.4%; Pred. No. 2e-77;

Matches 271; Conservative 115; Mismatches 242; Indels 137; Gaps 25;

Qy 39 MPRVRYAGDERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLK 98
:| | :| : | | | :| | | | : | | | | | : | : : | :
Db 28 VPRKTVSSGELVTVVRRESQTGIQDFLTTLTEHSGLLYVGAREALFAFSVE---ALELQ 84

Qy 99 NMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQD 158
| | | | | | | | | | | | | | | | | | :| | | | | | | :
Db 85 GAISWEAPAEKKIECTQKGKSNQTECFNFIRFLQPYNSSHLYVCGTYAFQPKCTYINM-- 142

Qy 159 SYLLPISEDKVMGKQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVL 218
: : :| | :| | | | :| | | | | | | | :| | | :| : : :
Db 143 -LTFTLDRAEFEDGKGKCPYDPAKGHTGLLVDGELYSATLNNFLGTPEVILRYMGTHHSI 201

Qy 219 KTDNFLRWLHHDASEV--AAIPST-----QVVYFFEETASEFDFFERLHTSRVARV 268

Db	202	KTEYLAFWL-NEPHFVGSFVPESVGSFTGDDDKIYFFFSERAVEYDCYSEQVVARVARV	260
Qy	269	CKNDVGG EKLLQKKWTTFLKAQLLCTQPG-QLPFNVIRHAVLLPADSPTAPHIYAVFTSQ	327
Db	261	CKGDMGGARTLQKKWTTFLKARLVCSAPDWKVYFNQLKAVHTLRGASWHNTTFFGVFQAR	320
Qy	328	WQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRTTYRGPETNPRPGSC-----SV	381
Db	321	W--GDMDLSAVCEYQLEQIQQVFEGPYKEYSEQAQKWARYTDPVPSPRPGSCINNWHRDN	378
Qy	382	GPSS-----DKALTFMKDHFLLMDEQV---VGTPLLVKSGVEYTRLAVETAQGLDGHSHLV	433
Db	379	GYTSSLELPDNTLNFIIKKHPLMEDQVKPRLGRPLLVKKNTNFTHVVADRVPGLDGATYTV	438
Qy	434	MYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVP	493
Db	439	LFIGTGDGWLKAVSLG-PWIHMVEELQVF-DQEPVESLVLSQSKKVLFA GSRSQLVQLS	496
Qy	494	RANCSVYESCVDCVLARDPHCAWDPESTRCCLLSA-----PNLNSWKQDMERGN	542
Db	497	LADCTKYRFCVDCVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYG-	555
Qy	543	PEWACASGPMSRSLRPQSRPQIIKEVLAVPNSI-----LELPCPHLSA-LASYWWSHG	594
Db	556	-----IKKVR SIPKNITVVS GTDLVLP C-HLSSNLAAHAWTFG	592
Qy	595	PAAVP--EASSTVYNGSLLLIV---QDGVGGLYQCWATENGFSYPVISYW---VDSQDQ	645
Db	593	SQDLPAEQPGSFLYDTGLQALVVMQAQSRHSGPYRCYEEQGTRLA AESYLVA VAGSSV	652
Qy	646	TLALDPELAGIPREHVKVPLTRVSGGAALAAQSYWPHFVTVTVL FALVLSGA----LII	701
Db	653	TL-----EARAPLENLG-----LVWLAVVALGAVCLVLLL	682
Qy	702	LVASPLRALRARGKVQCETLRPGEKA-----PLSREQHLQSP	739
Db	683	LVLSLRRRLR-----EELEKGAKASERTLVYPLELPKEPASP	719

RESULT 15

Q8BIC3

ID Q8BIC3 PRELIMINARY; PRT; 550 AA.

AC Q8BIC3;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732467N09 product:SEMAPHORIN 4B (SEMAPHORIN C) (SEMA C), full insert sequence.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AK028896; BAC26181.1; -.
DR HSSP; Q92854; 1OLZ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR011047; Quin_alc_DH_like.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
SQ SEQUENCE 550 AA; 61309 MW; 8C28E29DC4CAC958 CRC64;

Query Match 26.5%; Score 1067.5; DB 2; Length 550;
Best Local Similarity 42.7%; Pred. No. 1e-76;
Matches 233; Conservative 87; Mismatches 185; Indels 41; Gaps 14;

Qy 18 LFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDTLLLSGDGNTLY 77
| || ||| ||| | ||: | | | : | : : :: |||| || |||
Db 15 LLLLLLLLLLRTTTTRALG----PRISVPLGSEERLIRKFEAENISNYTALLLSQDGKTLY 70

Qy 78 VGAREAILALDIQDPGVP--RLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYN 135
|||||: ||: :| : :: | | :| :|:| | : | |:|:|:| |
Db 71 VGAREALFALNSNLSFLPGGEYQELL-WSADADRKQQCSFKGKDPKRDCQNYIKILLPLN 129

Qy 136 VTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVM--EGKGQSPFDPAHKHTAVLVDGML 193
: || |||| |||| | : | : | : ||: |||| | ||: ||| |
Db 130 SSHLLTCGTAAFSPLCAYIHIAFSTLAQDEAGNVILEDGKGRCFPDPNFKSTALVVDGEL 189

Qy 194 YSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAA-----IPSTQVV 243
|:|:|:| | |:| : | : | :| ||: | || | :||: | :
Db 190 YTGTVSSFQGNDAISRSQSSRPT-KTESSLNWL-QDPAFVASAYVPESLGSPIGDDDKI 247

Qy 244 YFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ-LPFN 302
|||| || ||: ||| ||||| || |||: ||: ||: ||||| :| |||
Db 248 YFFFSETGQEFEEFFENTIVSRVARVCKGDEGGERVLQQRWTSFLKAQLLCSRPDGDFPFN 307

Qy 303 VIRHAVLL---PADSPTAPHIYAVFTSQVQVGGTRSSAVCAFSLLDIERVFKGKYKELNK 359
|: : | | | | ||||| | ||: | |:| |:| :| | |:|:| :
Db 308 VLQDVFTLNPNPQDW-RKTLFYGVFTSQWHRGTTEGSAICVFTMNDVQKAFDGLYKKVNR 366

Qy 360 ETSRWTTYRGPETNPRPGSCSVGPS-----SDKALTFMKDHFLMDEQVVGTPLL 408
|| : | | ||||: | : | : | |:| ||||| || | ||
Db 367 ETQQWYTETHQVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVRSRLLL 426

Qy 409 VKSGVEYTRLAVETAQGLDGHS-HLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFDPDE 467
:: | |:| | | | : |:| || | |||| | |:| |:|:| :
Db 427 LQPRARYQRVAVHRVPGL--HSTYDVLFLGTGDGRLLHKAVTL-SSRVHIIIEELQIFPQGQ 483

Qy 468 PVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLS 527
|:|:| | | : | :| ||||: | :| |:| ||||: ||| : |
Db 484 PVQNLLLD SHGGLLYASSHSGVVQVPVANC SLYPTCGDCLLARDPYCAWTGSACRLASLY 543

Qy 528 APNLNS 533
|:| |

Db

544 QPDLAS 549

Search completed: February 10, 2005, 02:22:51
Job time : 222 secs